

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 11:49:29 ; Search time 9086 Seconds
(without alignments)
12574.588 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggtcgctggaccgaagc.....aaaaaaaaaaaaaaaaaaaa 3826

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estci:*
10: gb_estc2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vil:*
28: gb_gssi:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	878.2	23.0	1049	12	BM457033
2	793.4	20.7	835	14	CA310925
3	780.6	20.4	935	13	BQ069145
4	761.6	19.9	973	13	BQ879837

5	743.8	19.4	781	14	CB956370
6	730.8	19.1	789	14	CA444761
7	727.4	19.0	931	13	BU527114
8	701.8	18.3	906	13	BU171407
9	699.8	18.3	983	10	BE795637
10	697	18.2	2726	11	AK048725
11	696.4	18.2	785	14	CB960090
12	695.4	18.2	851	12	BG703589
13	690.2	18.0	768	9	AL554421
14	662.4	17.3	664	12	BM722392
15	657.4	17.2	922	14	CA984031
16	654.2	17.1	682	14	CA309985
17	645.2	16.9	766	13	BU612412
18	641.6	16.8	841	14	CF995034
19	634	16.6	634	12	BQ018441
20	632	16.5	632	12	BM994326
21	632	16.5	633	12	BM994326
22	600.2	15.7	762	12	BM946923
23	592.2	15.5	628	9	AU132503
24	587	15.3	776	13	BU121855
25	578.8	15.1	1018	13	BQ723205
26	568.2	14.9	661	13	BU611033
27	565.6	14.8	823	13	BU214796
28	563.8	14.7	732	9	AL554364
29	556.2	14.5	998	13	BU553767
30	547.4	14.3	705	10	BE258134
31	538.4	14.1	910	13	BM944120
32	535.4	14.0	717	12	BM950590
33	534.8	14.0	790	13	BU117232
34	531.2	13.9	893	13	BU412532
35	529.2	13.8	543	9	AW070327
36	522.6	13.7	698	13	BU222342
37	520.4	13.6	557	9	AU154016
38	519	13.6	519	9	AL138362
39	509	13.3	510	13	BM283437
40	506.2	13.2	749	10	BF696473
41	505.6	13.2	894	14	CF617275
42	500	13.1	512	9	AI681374
43	497.8	13.0	501	9	AL138363
44	495	12.9	507	10	BE315402
45	492.4	12.9	810	14	CB960174

ALIGNMENTS

RESULT 1
BM457033
LOCUS
DEFINITION
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cdna clone IMAGE:5583269
5', mRNA sequence.
ACCESSION
BM457033
VERSION
BM457033.1 GI:18506073
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1049)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12346 row: b column: 06
High quality sequence stop: 671.

BM457033 1049 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cdna clone IMAGE:5583269
5', mRNA sequence.

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FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5583269"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
Note: "Organ: Testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 23.0%; Score 878.2; DB 12; Length 1049;
Best Local Similarity 99.4%; Pred. No. 7e-121;
Matches 902; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 2386 CAGAGCATGGCCAGTAGTGTGGCAGCCGCAAGACACACAGCAGCAGCCTCTATGTCCCATGG 2445
Db 1 CAGAGCATGGCCAGTAGTGTGGCAGCCGCAAGACACACAGCAGCAGCCTCTATGTCCCATGG 60
QY 2446 CCTAAGACTTACCCCTGACCAAGCTAGTAGTGGGCCATTTACCCCTTGACCCAGTCCACA 2505
Db 61 CCTAAGACTTACCCCTGACCAAGCTAGTAGTGGGCCATTTACCCCTTGACCCAGTCCACA 120
QY 2506 GTGTGTACAGGTAGTACCTGTCTTAGGGTTGCTGTAGAGGCAACCTCTCTGTCCACCC 2565
Db 121 GTGTGTACAGGTAGTACCTGTCTTAGGGTTGCTGTAGAGGCAACCTCTCTGTCCACCC 180
QY 2566 CACACCAAGAACTATATGTCTTACTTCTCCACTGATCTGTGTGTCAGTGTATGATGCT 2625
Db 181 CACACCAAGAACTATATGTCTTACTTCTCCACTGATCTGTGTGTCAGTGTATGATGCT 240
QY 2626 GTGGCCTGTGAAGGCACTGTGTAGTGTGAGTCCACACATATAGTCATGTGCACCACT 2685
Db 241 GTGGCCTGTGAAGGCACTGTGTAGTGTGAGTCCACACATATAGTCATGTGCACCACT 300
QY 2686 TCCTGTCCACAGGCGGAGGAGGAGGAGGTGAGGGTATACCAAGCTGTATGACAGCCCAT 2745
Db 301 TCCTGTCCACAGGCGGAGGAGGAGGAGGTGAGGGTATACCAAGCTGTATGACAGCCCAT 360
QY 2746 AGCCTAAAGCAACTGACAGGACAGCCTCCCTGGATGATGATGATGATGATGATGATG 2805
Db 361 AGCCTAAAGCAACTGACAGGACAGCCTCCCTGGATGATGATGATGATGATGATGATG 420
QY 2806 ACAGAGTCCAGCAACCCCTCTTACGACAGGCTCTGTGACTGTGAGGTGCAGGAGGC 2865
Db 421 ACAGAGTCCAGCAACCCCTCTTACGACAGGCTCTGTGACTGTGAGGTGCAGGAGGC 480
QY 2866 TTCCAGAGCAGTGTGTGTATATTAGGACCCAGCACTGGGAGGGGCTGTGTGCTAGACCC 2925
Db 481 TTCCAGAGCAGTGTGTGTATATTAGGACCCAGCACTGGGAGGGGCTGTGTGCTAGACCC 540
QY 2926 CTTGTGACAGTGTGATCTATCTAGTGTAGTCTGTGCTGACAGAAACAGAGCCACTTG 2985
Db 541 CTTGTGACAGTGTGATCTATCTAGTGTAGTCTGTGCTGACAGAAACAGAGCCACTTG 600
QY 2986 TAGCTGTTTAAATAGACAAGGATTTACTACTGCGCCCTGTGTGCTGTGCAAAATTTGTG 3045
Db 601 TAGCTGTTTAAATAGACAAGGATTTACTACTGCGCCCTGTGTGCTGTGCAAAATTTGTG 660
QY 3046 GAAGAGCTGGAGAGCAGACTGTGTAATTTCCAGGAACCTCCAGGCGCAGATTCATCA 3105
Db 661 GAAGAGCTGGAGAGCAGACTGTGTAATTTCCAGGAACCTCCAGGCGCAGATTCATCA 720
QY 3106 TGTCTGTTGTGACAGGAAAGCTGCCCATCTCTGACGAAGCACTATGTCAGGAAGCTG 3165
Db 721 TGTCTGTTGTGACAGGAAAGCTGCCCATCTCTGACGAAGCACTATGTCAGGAAGCTG 780
QY 3166 CTGACTGCAGAACTAGGCT-CCCTCTGCCAGGTCCTGTCGCCAGCAATAGATGTCCTGAG 3224
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Db 781 CTGACTGCAGAACTAGGCTCCCTCTGCCAGGTCCTGCGAGCAATAGATGTCCTGAG 840
QY 3225 GCCTGCCCTCTCCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 3283
Db 841 GCCTGCCCTCTCCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 900
QY 3284 TTGGGGG 3290
Db 901 TTTGGGG 907

RESULT 2
CA310925 835 bp mRNA linear EST 04-NOV-2002
LOCUS UI-CF-FNO-afb-j-06-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
DEFINITION UI-CF-FNO-afb-j-06-0-UI 3', mRNA sequence.
ACCESSION CA310925
VERSION CA310925.1 GI:24529023
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 835)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers
1..835
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afb-j-06-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_ISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

ORIGIN
Query Match 20.7%; Score 793.4; DB 14; Length 835;
Best Local Similarity 99.3%; Pred. No. 3e-108;
Matches 827; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2039 row: g column: 20
High quality sequence stop: 708.
Location/Qualifiers
1. .935
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5803435"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: Brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match 20.4%; Score 780.6; DB 13; Length 935;
Best Local Similarity 98.4%; Pred. No. 2.4e-106;
Matches 820; Conservative 0; Mismatches 9; Indels 4; Gaps 3;

1618 TCAGTCTGGGTTCTGAAGCCTTCAGTAGTGGCTCCACTACTGCGAGGTGGTGGCG 1677
1 TCAGTCTGGGTTCTGAAGCCTTCAGTAGTGGCTCCACTACTGCGAGGTGGTGGCG 60

1678 GAGAAGACCCAGTGGGTGATCGGGTGGCACAGAGCCGCAAGCCGCAAGGCGCAGCATC 1737
61 GAGAAGACCCAGTGGGTGATCGGGTGGCACAGAGCCGCAAGCCGCAAGGCGCAGCATC 120

1738 CAGATCCAGCCAGCGCGGCTTCTACTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1797
121 CAGATCCAGCCAGCGCGGCTTCTACTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 180

1798 GCTGCAAGCCAGCGCTTGAAGCGGCTTAACTGCGGCAAGCTTCAAGGTCGATGTCGATGTCGATGTC 1857
181 GCTGCAAGCCAGCGCTTGAAGCGGCTTAACTGCGGCAAGCTTCAAGGTCGATGTCGATGTCGATGTC 240

1858 TTCCTGGACTATGACCAAGCTTGGCTCATCTTCAATGCTGATGATGATGCTGCTGCTGCTC 1917
241 TTCCTGGACTATGACCAAGCTTGGCTCATCTTCAATGCTGATGATGATGCTGCTGCTGCTC 300

1918 TACACCTCCGCGAGAGTTCCTGCGAGCTCTGCTTACTTCTAGCTGCGCCAGAGC 1977
301 TACACCTCCGCGAGAGTTCCTGCGAGCTCTGCTTACTTCTAGCTGCGCCAGAGC 360

1978 CAGCCCAATGGCAAGACCTTCAGCGCTGCGGATCAACACCGTCCGCTCTAGTCCAGG 2037
361 CAGCCCAATGGCAAGACCTTCAGCGCTGCGGATCAACACCGTCCGCTCTAGTCCAGG 420

2038 CAGAAGGAGACCAACCTCTCTGGGACCACTGCGCCACTGCAAGAGCCCTGCCAGGAAGA 2097
421 CAGAAGGAGACCAACCTCTCTGGGACCACTGCGCCACTGCAAGAGCCCTGCCAGG-AGA 479

2098 TAGAGAGCTGAGCTCCAGCCACCGTGGCCACTGAGAGCTCTGAGAGCTCTGAGAGCTGTTTACCC 2157
480 TAGAGAGCTGAGCTCCAGCCACCGTGGCCACTGAGAGCTCTGAGAGCTGTTTACCC 539

2158 TCCAGCTCCAGTCTGTAAATGGAGGTTCATCTCCTACTCTCTTAACTCTCTTCCAGC 2217

JOURNAL COMMENT
source
FEATURES
ORIGIN

2992 GTTTAATTAGACAGAGTTTACTACTGCGCCCTGTGCTTGCATAAAATTTTGGAGAG 3051
830 GTTTAATTAGACAGGA-TTACTACTGCGCCCTGGT-CTTTGCAAAATGNNTTGGAAGAG 773

3052 CTGGAGACGAGACTCTGCTGAATTTCCAGGAACCTCCAGGCGCAGATTTCATCATCTCG 3111
772 CTGGAGACGAGACTCTGCTG-ATTTCCAGGAACCTCCAGGCGCAGATTTCATCATCTCG 714

3112 TTGTGACCAAGGAAGCTGCCCATCTGCGAGAGCCACTATGCCAGAAAGCTGCTGACT 3171
713 TTGTGACCAAGGAAGCTGCCCATCTGCGAGAGCCACTATGCCAGAAAGCTGCTGACT 654

3172 GCAGAACTAGGCTCCCTCTGCGACAGCTGCGTGCAGCCTAATAGATGCTCTGAGGCTGCC 3231
653 GCAGAACTAGGCTCCCTCTGCGACAGCTGCGTGCAGCCTAATAGATGCTCTGAGGCTGCC 594

3232 CCTCTCCCACTTCACTCACTGCTCCCAATCTAAATTTTACAAGAGATTCTGTTGGGGGA 3291
593 CCTCTCCCACTTCACTCACTGCTCCCAATCTAAATTTTACAAGAGATTCTGTTGGGGGA 534

3292 ACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGA 3351
533 ACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGA 474

3352 AGGAAGTTAGGTTGGTGGAGCAGCCACCTGCGTTTTTCTGCCACAGATCCAAATCG 3411
473 AGGAAGTTAGGTTGGTGGAGCAGCCACCTGCGTTTTTCTGCCACAGATCCAAATCG 414

3412 TGAAGAACTCGGAGAGGTTGAGTCCATCTAGGTTTGTCTGCGCCCTTGGCTCTATC 3471
413 TGAAGAACTCGGAGAGGTTGAGTCCATCTAGGTTTGTCTGCGCCCTTGGCTCTATC 354

3472 CTTGCCACAGAGTTGGAACTGAGGAGTGGCTGCAAGACTGAGCCTAAATGTCCTCCCG 3531
353 CTTGCCACAGAGTTGGAACTGAGGAGTGGCTGCAAGACTGAGCCTAAATGTCCTCCCG 294

3532 GCTTTGACTTTTCTTTAGTCTGCGGCTAGATCTGCACTTGGGGTCTCTGACACAA 3591
293 GCTTTGACTTTTCTTTAGTCTGCGGCTAGATCTGCACTTGGGGTCTCTGACACAA 234

3592 CACACCATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGCTGCCCC 3651
233 CACACCATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGCTGCCCC 174

3652 CGCCACCGGGCTCCTTTGGGCAAAAGGAATGTCAGCCCTACCCCAACCCCTTCAACTA 3711
173 CGCCACCGGGCTCCTTTGGGCAAAAGGAATGTCAGCCCTACCCCAACCCCTTCAACTA 114

3712 CCAGATCTGGGCGCCACCCAGAGTATTTTATTTAAATGTTGCCATTTATGAGTTA 3771
113 CCAGATCTGGGCGCCACCCAGAGTATTTTATTTAAATGTTGCCATTTATGAGTTA 54

3772 TGATCAATTTGTTATTAATTTAAGTTACAGATGTCAAAAAATAAAAAA 3824
53 TGATCAATTTGTTATTAATTTAAGTTACAGATGTCAAAAAATAAAAAA 1

RESULT 3
BQ069145
LOCUS
DEFINITION
AGENCOURT_6738796 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5803435
S', mRNA sequence.
BQ069145
VERSION
BQ069145.1 GI:19898191
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 935)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)

stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCAATGC.

TAG_TISSUE=lung
TAG_LIB=UI-H-DH1
TAG_SEQ=AGATCAATGC

ORIGIN

Query Match 19.1%; Score 730.8; DB 14; Length 769;
Best Local Similarity 99.1%; Pred. No. 6.3e-99;
Matches 735; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3076 TTCAGGAATCCAGGCGCAGATCATCATGTCTGTGTGACAGAGAACTGCCCCCA 3135
DB 742 TTTCCAGAACTCCAGGCGCAGATTCATCATGTCTGTGTGACAGAGAACTGCCCCCA 683
QY 3136 TCTCAGGAAGCCACTATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCTCTGCCAC 3195
DB 682 TCTCAGGAAGCCACTATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCTCTGCCAC 623
QY 3196 GGTCCTGCGCAGCCAAATAGATGTCTTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCC 3255
DB 622 GGTCCTGCGCAGCCAAATAGATGTCTTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCC 563
QY 3256 AAATCTAAATTTTACAGAGATTCCTGTTGGGGAACTTAAGTCAGATCAGAACTTG 3315
DB 562 AAATCTAAATTTTACAGAGATTCCTGTTGGGGAACTTAAGTCAGATCAGAACTTG 503
QY 3316 GCTGCAAGGAGCTGCGGAATGTCATTCCTAGAGGAAGTTAGGCTGGTGGAGCA 3375
DB 502 GCTGCAAGGAGCTGCGGAATGTCATTCCTAGAGGAAGTTAGGCTGGTGGAGCA 443
QY 3376 GCGCCACCTCGTTTTCTGCCACAGCATCCAAATCGTGAAGAACTCGGGAGAGGGTGGAG 3435
DB 442 GCGCCACCTCGTTTTCTGCCACAGCATCCAAATCGTGAAGAACTCGGGAGAGGGTGGAG 383
QY 3436 TCCACATCTAGGTTGTCTGCCCTTGGCTCTATCCCTGCCAGAGGTGGAACTGGAG 3495
DB 382 TCCACATCTAGGTTGTCTGCCCTTGGCTCTATCCCTGCCAGAGGTGGAACTGGAG 323
QY 3496 GAGTGGGCTCAAGACTGAGCTTAAATGTCTCCCGGCTTGAATTTCTTCTAGTCCT 3555
DB 322 GAGTGGGCTCAAGACTGAGCTTAAATGTCTCCCGGCTTGAATTTCTTCTAGTCCT 263
QY 3556 GGGGCTTGTGCTGCACTTGGGTCTCTGACACACACACACATCCCAAGTAGCCGGAA 3615
DB 262 GGGGCTTGTGCTGCACTTGGGTCTCTGACACACACACACATCCCAAGTAGCCGGAA 203
QY 3616 GAGCTAAACACAGGGGTTCTTAAATGGTGGCTGCGCGGCTTGAATTTCTTCTAGTGGCA 3675
DB 202 GAGCTAAACACAGGGGTTCTTAAATGGTGGCTGCGCGGCTTGAATTTCTTCTAGTGGCA 143
QY 3676 AAAGGAATTCAGGCTTACCCCAACCCCTTCAACTACAGAAATCTGGGCGCACCCAGCAG 3735
DB 142 AAAGGAATTCAGGCTTACCCCAACCCCTTCAACTACAGAAATCTGGGCGCACCCAGCAG 83
QY 3736 TATTTTATTTAAATTTGTCCTTAAATGGTGGCTTGAATTTGATTAATTAAG 3795
DB 82 TATTTTATTTAAATTTGTCCTTAAATGGTGGCTTGAATTTGATTAATTAAG 23
QY 3796 TTACAGATGTCAAAAA 3817
DB 22 TTACAGAAAAA 1

RESULT 7

BUS27114

LOCUS

DEFINITION

10155963 NIH_MGC_101 Homo sapiens cDNA clone
IMAGE:6536868 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BUS27114
BUS27114.1 GI:22837555
Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapsb@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloning by: Agencourt Bioscience Corporation
Cloning distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2698 row: 0 column: 12
High quality sequence stop: 552.

FEATURES

Source

1. .931
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6536868"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site: 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 19.0%; Score 727.4; DB 13; Length 931;
Best Local Similarity 97.0%; Pred. No. 2e-98;
Matches 827; Conservative 0; Mismatches 16; Indels 10; Gaps 8;

QY 2100 GAGAGCTGAGCTCAGCCCAACCGTGGCCACTGGAGACCTCAGGCCAGTTGTTTACCCCTC 2159
DB 1 GAGAGCTGAGCTCAGCCCAACCGTGGCCACTGGAGACCTCAGGCCAGTTGTTTACCCCTC 60
QY 2160 CAGCTCCAGCTGTAATGAGGTTGCATTCCTACTTCTTAACTCTCTCCAGCAT 2219
DB 61 CAGCTCCAGCTGTAATGAGGTTGCATTCCTACTTCTTAACTCTCTCTCCAGCAT 120
QY 2220 CGATGTTCTGTAGCTCTGACCTTGTAGGATACAGCTTTGATCCAGGATGTGACATGG 2279
DB 121 CGATGTTCTGTAGCTCTGACCTTGTAGGATACAGCTTTGATCCAGGATGTGACATGG 180
QY 2280 CTTCTCTCAGGCAACCCCTGCCAACCCCTCATCCCATCTTCTCAGGGGCGAGGAGCT 2339
DB 181 CTTCTCTCAGGCAACCCCTGCCAACCCCTCATCCCATCTTCTCAGGGGCGAGGAGCT 240
QY 2340 ACCTTCCAGTGTCTCCTCCAGCCAGCCCTGACCTCAGGAAGTGTGACAGCATGGCCAG 2399
DB 241 ACCTTCCAGTGTCTCCTCCAGCCAGCCCTGACCTCAGGAAGTGTGACAGCATGGCCAG 300
QY 2400 TAGTTGGAGCCCGAAAGACACACAGACCCCTTATGTCCCATGAGCTTAAGCTTACCC 2459
DB 301 TAGTTGGAGCCCGAAAGACACACAGACCCCTTATGTGCCCTTACCTTACCTTACCC 360
QY 2460 CTGACCAAGCTAGTGTGGCCATTTACCTTACCCAGTCCACAGTGTGTACAGGTAG 2519
DB 361 CTGACCAAGCTAGTGTGGCCATTTACCTTACCCAGTCCACAGTGTGTACAGGTAG 420

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 983)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLC802 row: 9 column: 05

High quality sequence stop: 791.

FEATURES

source

1..983
/location/Qualifiers
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/clone="IMAGE:3944860"
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/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 18.3%; Score 699.8; DB 10; Length 983;
Best Local Similarity 97.3%; Pred. No. 2.5e-94;
Matches 787; Conservative 0; Mismatches 12; Indels 10; Gaps 7;
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DB 181 CTGCCACAGCCGAGGAGCAGGTTAGGGTATACCAAGCTGATGTCAGAGGCCATTAG 240
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DB 241 CTTAAAGCAACTGCAGGCAAGCCCTCCCTGGATGATGCGAGTCCCGAGTGTCTGAAC 300
QY 2808 AAGAGTCCAGCCCAACCTCTTCAGCCAGGCTCTGTGACCTGTAGGGTGCAGAGGCTT 2867
DB 301 AAGAGTCCAGCCCAACCTCTTCAGCCAGGCTCTGTGACCTGTAGGGTGCAGAGGCTT 360
QY 2868 CCAGAGCAGTTGTTGTAATTAGACCCAGCACTGGAGGGGCTGTGTGCTAGAGCCCT 2927
DB 361 CCAGAGCAGTTG-TGTAATTAGACCCAGCACTGGAGGGGCTGTGTGCTAGAGCCCT 419
QY 2928 TGTTCAGCTTGGCATCTATCTCAGTTAGGATCTCTGTGAGAGAAACAAGAGCCACTTGTA 2987
DB 420 TGTTCAGCTTGGCATCTATCTCAGTTAGGATCTCTGTGAGAGAAACAAGAGCCACTTGTA 479
QY 2988 GCTGGTTTAATTAGACAGGATTACTACTCTGGCCCTGGTGGCTTGCAAAATGTTGGA 3047

DB 480 GCTGGTTTAATTAGACAGGATTACTACTGGCCCTGGTGGCTTGCAAAATG-TGGA 538
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QY 3108 TCTGTTGTGACCAAGAAAGCTGCCCATCTGCGAGGAAGCCATATGCCAGAAAGCTGCT 3167
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QY 3228 TGCCCTCTCTCCACTTCACATCAGTTCCTCAATCTAAATTTTACAAGAGATTCCTGTTGG 3287
DB 717 TGGCCCTCTCCCA-TTCACATCAGTTCC-AAATCTAAATTTACACGAGATTCCTGTT-- 770
QY 3288 GGGAACTTAAGTCAGATCCAGAACCTTGG 3316
DB 771 GGGGAACCTTAGTCAGATCCAGAACCTTGG 799
RESULT 10
AK048725
LOCUS
DEFINITION
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:C230023D16 product:similar to CDNA FLJ10759
FIS, CLONE NT2RP3004617, WEAKLY SIMILAR TO ZINC-BINDING PROTEIN A33
[Homo sapiens], full insert sequence.
ACCESSION
AK048725.1 GI:26093070
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED
11042159
REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
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Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Iwata, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11076861
REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-690 (2001)
5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

TITLE
JOURNAL
REFERENCE
AUTHORS

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2726)
Fukuda, S., Furuno, M., Kimura, T., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Adachi, J., Aizawa, K., Hanagaki, T., Hara, A., Hashizume, W., Hayaehida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://phantom.gsc.riken.go.jp/
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ORIGIN

Query Match 18.2%; Score 697; DB 11; Length 2726;
Best Local Similarity 68.2%; Pred. No. 5.5e-94;
Matches 1201; Conservative 0; Mismatches 240; Indels 320; Gaps 4;

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DB |||||
QY 61 CCAGGTTTGGGCGCGGATCCGGCAGCTAGCGGGCCGGCACCCCTCTCTCTCTGCC 120
DB |||||
QY 85 CCGGATCTCGGCGCAGGTCGCGGAGCTGAGTGGCGCGGACCCCTCTCTCTGCC 144
DB |||||
QY 121 GGTACAGCAATGTACGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
DB |||||
QY 145 GGGCAAGCGCGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 204
DB |||||
QY 181 GTTCTCGCCCTCCCGCAGCGCCCGCCACCGGGATTTGGACCCCTTAAGGGCTCCAC 240
DB |||||
QY 205 GCTCGACCCCTCTCAAGCTTTTGGGTCCTGGGAT-----TCCGC 246
DB |||||
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DB |||||

247 CCCTCTTCGGGATCTCTCTCTCGCAGCATCTATCCCTTGGGAGTGTCTGTCTCTAGAT 306
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301 CTTCCCGGTGAGGATCTCGGTCCCTCAGCGCTCACAGCCTC---CTCCAGAGCGCCATC 357
DB |||||
307 CTTCTCTCGCTGGAGCCCTCTCTTGGGAGCGCTCGGCTCTCTCTCTCTCAGCGCCATC 366
QY |||||
358 GCGTTGAGCTGCCCATCTACTCTAGACTGCCCTCCCGGGTGGGTTGCCAGGAGTCTCA 417
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367 GCTGTGGGACCTTAGGATCTGAAACCGAGCTCCCGTGTCTGCATCCCGGGTGGCACC 426
QY |||||
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QY |||||
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DB |||||
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1126 GCAACTCCACCTCAAGTGTCTCTCTCTAGCAGCGCTGGTGGCTGTCTGGAGCT 1185
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1306 TTCAGACAGCGAGGGGAAACACACGAGCGCTCAGCTGTCAAGCGCACTGTTGGAG 1365

preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

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ORIGIN
Query Match      18.2%; Score 696.4; DB 14; Length 785;
Best Local Similarity 99.9%; Pred. No. 8.2e-94;
Matches 697; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 371 CACTACCTCTAGAGTGGCTCCCGGGGCTGGGCTCCACGGAGTCTCAGCGCGACCCCT 430
Db 28 CACTACCTCTAGAGTGGCTCCCGGGGCTGGGCTCCACGGAGTCTCAGCGCGACCCCT 87
QY 431 TCCTCGGTTTACCTCTCCGGACAGACACCCCTCTCTCTCCGGTAGTCTCTACCCCT 490
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QY 491 GCCTGTGCGGGCTCGTCCCGGGCCAGCCCTCGTGTCTCCGACAGCGCGCGCT 550
Db 148 GCCTGTGCGGGCTCGTCCCGGGCCAGCCCTCGTGTCTCCGACAGCGCGCGCT 207
QY 551 CTCTCAGCGCGCCCTCGCGCTCGCGCCCGCCCTCTCTCTCGCGCTGGCGCCATGGCT 610
Db 208 CTCTCAGCGCGCCCTCGCGCTCGCGCCCGCCCTCTCTCTCGCGCTGGCGCCATGGCT 267
QY 611 GCAGCCTCAAGGAGGAGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 670
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RESULT 12
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ACCESSION BG703589
VERSION BG703589.1 GI:13976072
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
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QY 3358 TTAGGCTGGTGGAGCAAGCCCACTCGCTTTTCTGCGCAGCATCCCAATCGTGAAGA 3417
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ACCESSION
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VERSION
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REFERENCE
  1 (bases 1 to 664)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
JOURNAL
  9704477
MEDLINE
  8889548
PUBMED
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
```

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
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/clone_lib="UI-E-800"
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UI-E-800 is a cDNA library containing the following
tissue(s): fetal eye. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCGTATACC. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 17.3%; Score 662.4; DB 12; Length 664;
Best Local Similarity 99.8%; Pred. No. 9.6e-89; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 1;

QY 311 AGGATCTCCGTCCTCAGCCGCTCACAGCCCTCTCCAGCGCCCATCGCTTGAGCTGCC 370
Db 1 AGGATCTCCGTCCTCAGCCGCTCACAGCCCTCTCCAGCGCCCATCGCTTGAGCTGCC 60

QY 371 CACTACCTCTAGACTGCGCTCCCGGGCTGGCGTCCCGAGAGTCTCAGCGCGCACCCCT 430
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QY 431 TCCTCGGTTTACCTCTTCGGACAGACACCCCTCTCGGTAGTCTCTACCCCT 490
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QY 491 GCCTGTGCGGCTCTGCTCCCGCGCCAGCCCTCGGTCTGCTCCGACAGCGCGGCT 550
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QY 551 CTCTCAGCGCGCTCTGCTCCCGCGCCCTCTCTGCTGCGCCCTGGCGCATGGGT 610
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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mouse embryonic limb, maxilla and mandible, day 10.5 and
11.5 (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp, Average insert size 1.8k bp. Priming sequence:
5'-GACTAGTTCTTAGATCGAGCGCGCC(T) 3'. Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp."
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GenCore version 5.1.6
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and is derived by analysis of the total score distribution.

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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Killary,A., Chandler,D. and Lott,S.				
TITLE	The tumor suppressor car-1				
JOURNAL	Patent: WO 0212285-A 3 14-FEB-2002;				

BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)

FEATURES

source

Location/Qualifiers
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RESULT 2

AX877131
LOCUS AX877131
DEFINITION Sequence 12036 from Patent EP1074617.
ACCESSION AX877131
VERSION AX877131.1 GI:40031867
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, I., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 12036 07-FEB-2001;
Research Association for Biotechnology (JP)
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ORIGIN

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Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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AK001621 3436 bp mRNA linear PRI 01-AUG-2002
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AK001621
AK001621.1 GI:7022986
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Isogai, T., Ota, T., Hayaishi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimori, K.,
Tanai, H., Kimata, M., Watanabe, M., Hirooka, S., Ishii, S., Kawai, Y.,
Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K.,
Masuho, Y. and Kanehori, K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3436)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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ORIGIN

Query Match 82.7%; Score 3163; DB 9; Length 3436;
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2	Srausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shermen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Casavant, T.L., Abrancini, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Carranson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Ia, X., Gibbs, R.A., Fahy, J., Heiton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
3	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
4	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
5	22388257		
6	12477932		
7	2 (bases 1 to 3259)		
8	Srausberg R.		
9	Direct Submission		
10	Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
11	NIH-MGC Project URL: http://mgc.nci.nih.gov		
12	Contact: MGC help desk		
13	Email: cgapsb@mail.nih.gov		
14	Tissue Procurement: ATCC		
15	cDNA Library Preparation: Rubin Laboratory		
16	DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
17	cDNA Sequencing by: Genome Sequence Centre.		

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BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Ling Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Mirandaa Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 6 Row: J Column: 17
This clone was selected for full length sequencing because it
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2999 Db CACTTGGGCTCTCTGACACAACACACCATCCCAAAGTAGCCGAGAGCTAAACACAGGG 3058
3631 QY GGTTCCTTAAATGGCTGCCCGCCACCGGGCTCCCTTGGGCAAGAAATGTCAGC 3690
3059 Db GGTTCCTTAAATGGCTGCCCGCCACCGGGCTCCCTTGGGCAAGAAATGTCAGC 3118
3691 QY CTTACCCCAACCTTCAACTAGCAGAACTCTGGGCCACCCACAGCAGTATTTTATTTAAA 3750
3119 Db CTTACCCCAACCTTCAACTAGCAGAACTCTGGGCCACCCACAGCAGTATTTTATTTAAA 3178
3751 QY TGTGGCCATTTTATGATTTATGATCAATTTGTAATAAATAAGTTACAGATGTCAAAA 3810
3179 Db TGTGGCCATTTTATGATTTATGATCAATTTGTAATAAATAAGTTACAGATGTCAAAA 3238
3811 QY AAAAAAATAAAAAA 3826
3239 Db AAAAAAATAAAAAA 3254

RESULT 6

BC007999

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

BC007999 3259 bp mRNA linear PRI 03-OCT-2003
Homo sapiens hypothetical protein FLJ10759, mRNA (cdna clone
MGC:15757 IMAGE:3357436), complete cds.
BC007999
BC007999.1 GI:14124949
MGC.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1. (bases 1 to 3259)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22389257
PUBMED	12477932
REFERENCE	2. (bases 1 to 3259)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (15-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalios, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IPAL Plate: 23 Row: a Column: 20. Location/Qualifiers 1..3259 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:15757 IMAGE:3357436" /tissue_type="Eye, retinoblastoma" /clone_lib="NIH_MGC_16" /lab_host="DH10B-R" /note="Vector: pOTB7" 1..3259 /gene="FLJ10759" /db_xref="LocusID:55223" 34..1461 /codon_start=1 /product="hypothetical protein FLJ10759" /protein_id="AAH07999.1"

QY	1231	GACATCGAGCAGAAAGTCCAGCGCTACAGCCAGCAGCTGCGCAAGTTC	CAGGAGGAGCC	1239
DB	661	GACATCGAGCAGAAAGTCCAGCGCTACAGCCAGCAGCTGCGCAAGTTC	CAGGAGGAGCC	720
QY	1291	CAGATCTCGCAGGAGCGGCTGGCTGAACCCGACCGGCACACCTTCTCTGGCTGGGGTGGCC	1350	
DB	721	CAGATCTCGCAGGAGCGGCTGGCTGAACCCGACCGGCACACCTTCTCTGGCTGGGGTGGCC	780	
QY	1351	TCATGTCCGAGCGGCTCAAGGGAAATAATCATGAGACCAACTTCAATATGAAGACTTC	1410	
DB	781	TCATGTCCGAGCGGCTCAAGGGAAATAATCATGAGACCAACTTCAATATGAAGACTTC	840	
QY	1411	CCGACCTCCAAAGTACACAGGCGCCCTGCAGTACACCATCTGGAAGTCCCTGTTCCAGGAC	1470	
DB	841	CCGACCTCCAAAGTACACAGGCGCCCTGCAGTACACCATCTGGAAGTCCCTGTTCCAGGAC	900	
QY	1471	ATCCACCCAGTGCAGCGGCCCTAACTTGGACCCGGGCACAGCCACCAAGCGCTGATC	1530	
DB	901	ATCCACCCAGTGCAGCGGCCCTAACTTGGACCCGGGCACAGCCACCAAGCGCTGATC	960	
QY	1531	CTGTCCGAGCACTGCACATCTGTGGCTTACGGCAATTGCAACCCACAGCCACTGCAGGAC	1590	
DB	961	CTGTCCGAGCACTGCACATCTGTGGCTTACGGCAATTGCAACCCACAGCCACTGCAGGAC	1020	
QY	1591	TCGCCAAAGCGCTTCGATGTGGAGCTCTGGTGCTGGGTTCTGAAGCCTTCAGTAGTGGC	1650	
DB	1021	TCGCCAAAGCGCTTCGATGTGGAGCTCTGGTGCTGGGTTCTGAAGCCTTCAGTAGTGGC	1080	
QY	1651	GTCCACTACTGGGAGTGGTGGTGGCGGAGAAAGCCAGTGGGTGATCGGGCTTGGCACAC	1710	
DB	1081	GTCCACTACTGGGAGTGGTGGTGGCGGAGAAAGCCAGTGGGTGATCGGGCTTGGCACAC	1140	
QY	1711	GAAGCCGCAAGCCGCAAGGCGAGATCCAGATCCAGCCGAGCGGGTCTTACTGCATC	1770	
DB	1141	GAAGCCGCAAGCCGCAAGGCGAGATCCAGATCCAGCCGAGCGGGTCTTACTGCATC	1200	
QY	1771	GTGATGACCATGGCAACCAAGTACAGCGCTGCACGAGCCCTGAGCGGGCTTACGTC	1830	
DB	1201	GTGATGACCATGGCAACCAAGTACAGCGCTGCACGAGCCCTGAGCGGGCTTACGTC	1260	
QY	1831	CGGGAACAGCTTGACAAAGTGGGTGTTCTCTGGACTATGACCAAGGCTTGCTCATCTTC	1890	
DB	1261	CGGGAACAGCTTGACAAAGTGGGTGTTCTCTGGACTATGACCAAGGCTTGCTCATCTTC	1320	
QY	1891	TACAATGCTCATACATGTCCTGGCTTACACCTTCGGCGAGAGTTCCCTGGCAAGCTC	1950	
DB	1321	TACAATGCTCATACATGTCCTGGCTTACACCTTCGGCGAGAGTTCCCTGGCAAGCTC	1380	
QY	1951	TGCTCTTACTTCAGCCCTGGCCAGAGCCACGCAATGGCAAGACTTCAGCGCGTGGG	2010	
DB	1381	TGCTCTTACTTCAGCCCTGGCCAGAGCCACGCAATGGCAAGACTTCAGCGCGTGGG	1440	
QY	2011	ATCAACACCGTCCGATCTAGTCCAGGCAAGAGAGACCAACCTCTGGGACCACTGC	2070	
DB	1441	ATCAACACCGTCCGATCTAGTCCAGGCAAGAGAGACCAACCTCTGGGACCACTGC	1500	
QY	2071	CACCTCGAAGAGCCCTGCCAGGAGATAGACCTGACCTCCAGCCACCGTGGCCAC	2130	
DB	1501	CACCTCGAAGAGCCCTGCCAGGAGATAGACCTGACCTCCAGCCACCGTGGCCAC	1559	
QY	2131	TGGAGACCTTCAGCCAGTTGTTTACCCCTCCAGCCTCCAGTCTGTAATAATGGAGTTGCAT	2190	
DB	1560	TGGAGACCTTCAGCCAGTTGTTTACCCCTCCAGCCTCCAGTCTGTAATAATGGAGTTGCAT	1619	
QY	2191	TCCTTACTTCTTAACTCTTCTCCAGCATCGAATGTTCTAGCTCTGACTTGATAGGGA	2250	
DB	1620	TCCTTACTTCTTAACTCTTCTCCAGCATCGAATGTTCTAGCTCTGACTTGATAGGGA	1679	
QY	2251	TACAGCTTTGATCCAGGATGACATGCTTCTCCTCAGGCAACCCCTGCCAACCTT	2310	
DB	1680	TACAGCTTTGATCCAGGATGACATGCTTCTCCTCAGGCAACCCCTGCCAACCTT	1739	

QY	2311	CATCCCCATCTCTCTCAGGGGACAGGGGACTACTCTTCCAGTGTCTCCCTCCAGCCAGCCGCGCT	2370
Db	1740	CATCCCCATCTCTCTCAGGGGACAGGGGACTACTCTTCCAGTGTCTCCCTCCAGCCAGCCGCGCT	1799
QY	2371	GACCTCAGGAAGTGTACAGACATGGCCAGTAGTGTGGCAGCCCGGAAAGACACACAGACCC	2430
Db	1800	GACCTCAGGAAGTGTACAGACATGGCCAGTAGTGTGGCAGCCCGGAAAGACACACAGCA-CC	1858
QY	2431	TCTTATGTCCCATGCCCTAAAGACTTACCCCTGACCAAGCTAGTGTGATGGGCCATTTACCGCT	2490
Db	1859	TCTTATGTCCCATGCCCTAAAGACTTACCCCTGACCAAGCTAGTGTGATGGGCCATTTACCGCT	1918
QY	2491	TGACCCCGAGTCCACAGTGGTACAGGTAGTACCTGGTCTTAGGGTTCGCTGAGAGCCCAAC	2550
Db	1919	TGACCCCGAGTCCACAGTGGTACAGGTAGTACCTGGTCTTAGGGTTCGCTGAGAGCCCAAC	1978
QY	2551	CTCTCCTGCCACCCCCACACCAAGAACTATATGTGTTCTACTTCTCCCACTGATCTGCTG	2610
Db	1979	CTCTCCTGCCACCCCCACACCAAGAACTATATGTGTTCTACTTCTCCCACTGATCTGCTG	2038
QY	2611	GTCACTGATGATGCTGTGGCTGTGGGAAGGCACCTGTTAGTGTAGTCCCACTGATCTGCTG	2670
Db	2039	GTCACTGATGATGCTGTGGCTGTGGGAAGGCACCTGTTAGTGTAGTCCCACTGATTTAGT	2098
QY	2671	CATGTGCCACACCTTCTCTGCCACAGGCCGAGGACAGGGTGAAGGTATACCCAAAGCT	2730
Db	2099	CATGTGCCACACCTTCTCTGCCACAGGCCGAGGACAGGGTGAAGGTATACCCAAAGCT	2158
QY	2731	GATGCAGAGCCCATTAGCCTAAAGGAACTGTCAGGACAAGCCTCCCTGGGATGTCAGGT	2790
Db	2159	GATGCAGAGCCCATTAGCCTAAAGGAACTGTCAGGACAAGCCTCCCTGGGATGTCAGGT	2218
QY	2791	CCCAGTAGCTCTGAAACAAGAGTCCAGCCAAACCTCTTTCAGCCAGAGCCTCTGTGACCTGC	2850
Db	2219	CCCAGTAGCTCTGAAACAAGAGTCCAGCCAAACCTCTTTCAGCCAGAGCCTCTGTGACCTGC	2278
QY	2851	TAGGGTGCAGGAGCTTTCAGAAAGCAGTTGTGTAAATTAGGACCCAGCACTGGGAGGG	2910
Db	2279	TAGGGTGCAGGAGCTTTCAGAAAGCAGTTGTGTAAATTAGGACCCAGCACTGGGAGGG	2338
QY	2911	CTGTTGGCTAGACCCCTTGTACAGCTTGGCATCTATCTCAGTTAGGATCTGCTGCAGAA	2970
Db	2339	CTGTTGGCTAGACCCCTTGTACAGCTTGGCATCTATCTCAGTTAGGATCTGCTGCAGAA	2398
QY	2971	AACAAGAGCCACTTGTAGCTGGTTTAAATAGACAAGGATTTACTACTGGCCCTGGTGG	3030
Db	2399	AACAAGAGCCACTTGTAGCTGGTTTAAATAGACAAGGATTTACTACTGGCCCTGGTGG	2458
QY	3031	CTTGCAAAAATTGTTGGAAGAGCTGGGAAGCAGACTCTGCTGAATTTCCAGGAACTCCCA	3090
Db	2459	CTTGCAAAAATTGTTGGAAGAGCTGGGAAGCAGACTCTGCTGNAATTTCCAGGAACTCCCA	2518
QY	3091	GCGCCGATTCATCATGTCTGTTGTACACAGGAAAGCTGCCCCCATCTGCAGGAAGCCAC	3150
Db	2519	GCGCCGATTCATCATGTCTGTTGTACACAGGAAAGCTGCCCCCATCTGCAGGAAGCCAC	2578
QY	3151	TATGCCAGAAAGCTGCTGACTGCAGAAACTAGGCTCCCTCTGCACAGGTCGGTCCAGCCA	3210
Db	2579	TATGCCAGAAAGCTGCTGACTGCAGAAACTAGGCTCCCTCTGCACAGGTCGGTCCAGCCA	2638
QY	3211	ATGATGTCTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCCAAAATCTAAATTTTATA	3270
Db	2639	ATGATGTCTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCCAAAATCTAAATTTTATA	2698
QY	3271	CAGAGATCTGTTTGGGGAACTTAAGTCAGATCCAGAACCTTGGCTGCAGGGAGTCT	3330
Db	2699	CAGAGATCTGTTTGGGGAACTTAAGTCAGATCCAGAACCTTGGCTGCAGGGAGTCT	2758
QY	3331	GGGAAATGTCATTTCCCTAGAGGAAGTTAGGCTGGGTGGAGCAAGCCCACTTCGGTTT	3390
Db	2759	GGGAAATGTCATTTCCCTAGAGGAAGTTAGGCTGGGTGGAGCAAGCCCACTTCGGTTT	2818
QY	3391	TTCTGCCACAGCATCCAAATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTTAGGTT	3450

ORIGIN	Receptor. " /db_xref="CDD:smart00449"									
	Query Match	78.8%;	Score 3014;	DB 9;	Length 3259;					
	Best Local Similarity	99.9%;	Pred. No. 0;							
	Matches 3254;	Conservative	0;	Mismatches	0;	Indels	2;	Gaps	2;	
QY	571	CCTCGGCCCCCCTCTCTGCTGCCCCCTTGCGCCCATGGCGTGCAGCCTCAAGGACGAGCTG	630							
Db	1	CCTCGGCCCCCCTCTCTGCTGCCCCCTTGCGCCCATGGCGTGCAGCCTCAAGGACGAGCTG	60							
QY	631	CTGTGCTCCATCTGCTGTAGACATCTACAGAACCGGTGAGCCTTGGGTGCGAGCACTAC	690							
Db	61	CTGTGCTCCATCTGCTGTAGACATCTACAGAACCGGTGAGCCTTGGGTGCGAGCACTAC	120							
QY	691	TTTCGCCGCGCTGCATCACGGAGCACTGGGTGGCGAGGAGCGCAGGCGCCCGCGAC	750							
Db	121	TTTCGCCGCGCTGCATCACGGAGCACTGGGTGGCGAGGAGCGCAGGCGCCCGCGAC	180							
QY	751	TGCCCCAGAGTGCCGCGCAGTTCGCGGAGCCCGCTGGCGGCCAGCCTCAAGCTGGCC	810							
Db	181	TGCCCCAGAGTGCCGCGCAGTTCGCGGAGCCCGCTGGCGGCCAGCCTCAAGCTGGCC	240							
QY	811	AACATCGTGAAGCGCTACAGCTCCTTCCGCTGGAACGCACTCTCAACGCGCGCCGCC	870							
Db	241	AACATCGTGAAGCGCTACAGCTCCTTCCGCTGGAACGCACTCTCAACGCGCGCCGCC	300							
QY	871	GCGGACCTTGCAGGCGCAGCAAGTCAAGCTCTTCTGCCTCAGGACCGGCGCCTT	930							
Db	301	GCGGACCTTGCAGGCGCAGCAAGTCAAGCTCTTCTGCCTCAGGACCGGCGCCTT	360							
QY	931	CTCTGCTTCTTGCAGAGCCTTGCACAGCAGCATCAGGTCAACGCGCATCGAC	990							
Db	361	CTCTGCTTCTTGCAGAGCCTTGCACAGCAGCATCAGGTCAACGCGCATCGAC	420							
QY	991	GAGCCTTCGAGCTGCGAGGAGCTGAAAGCAAACTTCAGGCCCCCTTCAAGACAGC	1050							
Db	421	GAGCCTTCGAGCTGCGAGGAGCTGAAAGCAAACTTCAGGCCCCCTTCAAGACAGC	480							
QY	1051	GAGGGGAACACACCGAAGCGCTGCAGCTGCTCAAGGCAAACTGGCGGAGACCAAGTCT	1110							
Db	481	GAGGGGAACACACCGAAGCGCTGCAGCTGCTCAAGGCAAACTGGCGGAGACCAAGTCT	540							
QY	1111	TCCACCAAGAGCCTTCGCGAACCACTATCGGCGAGGCGCTTCGAGCGGCTGCACCGCTGCTG	1170							
Db	541	TCCACCAAGAGCCTTCGCGAACCACTATCGGCGAGGCGCTTCGAGCGGCTGCACCGCTGCTG	600							
QY	1171	CGTGAACGCGCAGAAAGCCATGCTAGAGAGCTGGAGCGGACACCGGCCCGCAGCTGACC	1230							
Db	601	CGTGAACGCGCAGAAAGCCATGCTAGAGAGCTGGAGCGGACACCGGCCCGCAGCTGACC	660							
QY	1231	GACATCGAGCAGAAAGTCCAGCGCTACAGCCAGCAGCTGCGAAGTTCAGGAGGAGCC	1290							
Db	661	GACATCGAGCAGAAAGTCCAGCGCTACAGCCAGCAGCTGCGAAGTTCAGGAGGAGCC	720							
QY	1291	CAGATCCTGCGAGGCGGCTGGCTGAAACCGACCGGCACACCTTCTTGGCTGGGGTGGCC	1350							
Db	721	CAGATCCTGCGAGGCGGCTGGCTGAAACCGACCGGCACACCTTCTTGGCTGGGGTGGCC	780							
QY	1351	TCACTGTCCGAGCGGCTCAAGGAAAAATCCATGAGACCAACCTCAATATGAAGACTTC	1410							
Db	781	TCACTGTCCGAGCGGCTCAAGGAAAAATCCATGAGACCAACCTCAATATGAAGACTTC	840							
QY	1411	CCGACCTCGAAGTACACAGSCCCCGCTGCAGTACACATCTGGAAGTCCCTGTTCCAGGAC	1470							
Db	841	CCGACCTCGAAGTACACAGSCCCCGCTGCAGTACACATCTGGAAGTCCCTGTTCCAGGAC	900							
QY	1471	ATCCACCCAGTGCAGCGGCCCTAAACCTTGACCCCGGGCACAGCCACAGCGCCTGATC	1530							
Db	901	ATCCACCCAGTGCAGCGGCCCTAAACCTTGACCCCGGGCACAGCCACAGCGCCTGATC	960							
QY	1531	CTGTGGAAGCATGCGACCAATTGTGGCTTACGGCAACTTGACCCACAGGCACATGCAAGGAC	1590							

Db	2039	GTCACTGATGATGCTGTGGGCTGTGGAGGACCTGGTAGTGTGAGTCCACACATTAAGT	2098
QY	2671	CAFTGCGCCACCACTTCTGCCCAACAGCCGAGGACAGGGTGAAGGTATACCAAGCT	2730
Db	2099	CATGTGCCACCACTTCTGCCCAACAGCCGAGGACAGGGTGAAGGTATACCAAGCT	2158
QY	2731	GATGACAGAGCCATTAGCTTAAGCAACTGCAGGACAAGCCCTCCCTGGATGATCGAGGT	2790
Db	2159	GATGACAGAGCCATTAGCTTAAGCAACTGCAGGACAAGCCCTCCCTGGATGATCGAGGT	2218
QY	2791	CCCAGTAGCTCTGAAACAAGAGTCCAGCCACCCCTCTTCAGCCAGGCTCTGTGACCTGC	2850
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QY	2851	TAGGGTCAGAGAGCTTCCAGAACAGTGTGTGTAATTAGAACCCAGACACTGGAGGGG	2910
Db	2279	TAGGGTCAGAGAGCTTCCAGAACAGTGTGTGTAATTAGAACCCAGACACTGGAGGGG	2338
QY	2911	CTGTGGCTAGACCCCTTGTGACACTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAA	2970
Db	2339	CTGTGGCTAGACCCCTTGTGACACTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAA	2398
QY	2971	AACAAGAGCCACTGTAGCTGTTTAAATTAGACAAGGATTTACTACCTGGCCCCCTGGTG	3030
Db	2399	AACAAGAGCCACTGTAGCTGTTTAAATTAGACAAGGATTTACTACCTGGCCCCCTGGTG	2458
QY	3031	CTTGCAAAATTTGGAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAATCTCCA	3090
Db	2459	CTTGCAAAATTTGGAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAATCTCCA	2518
QY	3091	CGCGCAGATTCATCATGCTGTGTGACAGGAAGCTGCCCATCTGCAAGGAGCCAC	3150
Db	2519	CGCGCAGATTCATCATGCTGTGTGACAGGAAGCTGCCCATCTGCAAGGAGCCAC	2578
QY	3151	TATGCCAGAAAGCTGCTGACTGCAGAACTAGGCTCCCTCTGCCAGGCTCCGCGCCAC	3210
Db	2579	TATGCCAGAAAGCTGCTGACTGCAGAACTAGGCTCCCTCTGCCAGGCTCCGCGCCAC	2638
QY	3211	ATAGATGCTGAGGCTGCCCTCTCCACTTCACTCAGTCCCAATCTCAATTTTAA	3270
Db	2639	ATAGATGCTGAGGCTGCCCTCTCCACTTCACTCAGTCCCAATCTCAATTTTAA	2698
QY	3271	CAAGAGATTCCTGTTGGGGAACTTAAGTCAGATCCAGAACTTGGCTGCAAGGAGTCT	3330
Db	2699	CAAGAGATTCCTGTTGGGGAACTTAAGTCAGATCCAGAACTTGGCTGCAAGGAGTCT	2758
QY	3331	GGGAAATCTATTTCCCTAGAGGAAGTTAGGTTGGGTGGAGCAAGCCACCTCGGTTT	3390
Db	2759	GGGAAATCTATTTCCCTAGAGGAAGTTAGGTTGGGTGGAGCAAGCCACCTCGGTTT	2818
QY	3391	TTCTGCCACAGATCCAACTGTAAGAACTCGGGAGAGGTTGGAGTCCACATCTAGGGTT	3450
Db	2819	TTCTGCCACAGATCCAACTGTAAGAACTCGGGAGAGGTTGGAGTCCACATCTAGGGTT	2878
QY	3451	GTCTGCCCCCTGGCTCTATCCCTGCCAGAGTGGGAACCTGGAGAGTGGGCTCAAGA	3510
Db	2879	GTCTGCCCCCTGGCTCTATCCCTGCCAGAGTGGGAACCTGGAGAGTGGGCTCAAGA	2938
QY	3511	CTGAGCTTAAATGTCTCCCGGCTTGAATTTTCTTTCTAGTCTGGGGCTTAGATCTG	3570
Db	2939	CTGAGCTTAAATGTCTCCCGGCTTGAATTTTCTTTCTAGTCTGGGGCTTAGATCTG	2998
QY	3571	CACTTGGGGTCTCTGACACACACACCACTCCCAAGTAGCCGGAAGAGCTAAACACAGG	3630
Db	2999	CACTTGGGGTCTCTGACACACACACCACTCCCAAGTAGCCGGAAGAGCTAAACACAGG	3058
QY	3631	GGTTCTTAAATGGTGTGCCCGCCCAACCGGGCTCCCTTTGGGCAAGAAATGTCAGC	3690
Db	3059	GGTTCTTAAATGGTGTGCCCGCCCAACCGGGCTCCCTTTGGGCAAGAAATGTCAGC	3118
QY	3691	CTACCCCAACCTTCACTACAGAACTCTGGGCCACCCACAGTATTTTATTAA	3750
Db	3119	CCTACCCCAACCTTCACTACAGAACTCTGGGCCACCCACAGTATTTTATTAA	3178

QY	3751	TGTTGCCATTTTATGATCAATTTGTTAAATTTAAAGTTTACAGATGTCAAAA	3810
Db	3179	TGTTGCCATTTTATGATCAATTTGTTAAATTTAAAGTTTACAGATGTCAAAA	3238
QY	3811	AAAAAAAAAAAAAAAA 3826	
Db	3239	AAAAAAAAAAAAAAAA 3254	

BC012152

3259 bp

linear

PRI 04-OCT-2003

LOCUS

MG:20370 IMAGE:4558639, complete cds.

ACCESSION

BC012152

VERSION

BC012152.1

GI:15082475

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 3259)

STRAUSBERG, R.L., FEINGOLD, E.A., GROUSE, L.H., DERGE, J.G., KLAUSNER, R.D., COLLINS, F.S., WAGNER, L., SHENMEN, C.M., SCHULER, G.D., ALTSCHUL, S.F., ZEEBERG, B., BUETOW, K.H., SCHAEFER, C.F., BHAT, N.K., HOPKINS, R.F., JORDAN, H., MOORE, T., MAX, S.I., WANG, J., HSIEH, F., DIATCHENKO, L., MARUSINA, K., FARMER, A.A., RUBIN, G.M., HONG, L., SCAPLETON, M., SOARES, M.B., BONALDO, M.F., CASAVANT, T.L., SCHEETZ, T.E., BROWNSTEIN, M.J., USIDIN, T.B., TOSHIYUKI, S., ARMINCI, P., PRANGE, C., RAHA, S.S., LOQUELLANO, N.A., PETERS, G.J., CARMON, R.D., MULLAHY, S.J., BOSAK, S.A., MCEWAN, P.J., MCKERNAN, K.J., MALEK, J.A., GUNARATNE, P.H., RICHARDS, S., WOLEY, K.C., HALE, S., GARCIA, A.M., GAY, L.J., HULKY, S.W., VILLALON, D.K., MUZY, D.M., SODERGREN, E.J., LU, X., GIBBS, R.A., FAHEY, J., HELTON, E., KETTEMAN, M., MADAN, A., RODRIGUES, S., SANCHEZ, A., WHITING, M., MADAN, A., YOUNG, A.C., SHEVCHENKO, Y., BOUFFARD, G.C., BLAKESLEY, R.W., TOUCHMAN, J.W., GREEN, E.D., DICKSON, M.C., RODRIGUEZ, A.C., GRIMWOOD, J., SCHMUTZ, J., MYERS, R.M., BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALSKA, U., SMAILUS, D.E., SCHNERCH, A., SCHEIN, J.E., JONES, S.J. and MARRA, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 3259)

STRAUSBERG, R.

Direct Submission

Submitted (02-AUG-2001)

National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Iliisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spencer, Jeff Stott, Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 29 Row: d Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922647.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
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1 Matsuda, A. and Muramatsu, S.			
AUTHORS			
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RESULT 10

AK122896

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AK122896

3148 bp

mRNA

linear

PRI 09-SEP-2003

Homo sapiens cDNA FLJ16558 fis, clone SYN04001153, weakly similar to Zinc-binding protein A33.

AK122896

GI:34528340

oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1

Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 3148)

Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail: genomics@hri.co.jp, tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers

1..3148

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Query Match 68.8%; Score 2631; DB 9; Length 3148;

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LOCUS
DEFINITION Sequence 7 from Patent WO0212285.
ACCESSION AX491283
VERSION AX491283.1 GI:22323984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Killary,A., Chandler,D. and Lott,S.
AUTHORS The tumor suppressor car-1
TITLE Patent: WO 0212285-A 7 14-FEB-2002;
JOURNAL BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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QY	2738	AGGCCATTAGCCTAAAGCAACTGCAGGA	CAAGCCCTCCCTGGATGATCGAGGTCCCCAGT	2797
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Db	13848	AGTCTCTGAAACAAGATCCAGGCAACCTCTT	CAGCCAGAGCCTCTGTGACCTCTGTAGGGTG	13907
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Db	13968	CTAGACCCCTTGTCTAGACTTGGCACTATCTCT	CAGTTAGGATCCTGCTGCAGAAAACAAGA	14027
QY	2978	GCCACTTGTAGCTGTTTAAATTAGACAAGATTTA	CTACTGGCCCTCTGGTGGCTTGCAG	3037
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QY	3578	GGTCTCTGACACAACACACCACTCCCAAGTAG	CCGGAAGACTTAAACACAGGGGGTTCTTT	3637
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Db	14688	AAAAATGGCTGCCCGCCCAACCGGGCTCTCC	TCTGGGCAAAAGGAATGTCCAGCCCTACCC	14747
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RESULT 14
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DEFINITION Sequence 8 from Patent WO0212285.
ACCESSION AX491284
VERSION AX491284.1 GI:22323985
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SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Killary,A., Chandler,D. and Lott,S.
TITLE The tumor suppressor car-1
JOURNAL Patent: WO 0212285-A 8 14-FEB-2002;
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RESULT 15

AX775829

LOCUS

AX775829 2246 bp mRNA linear PAT 14-JUL-2003

DEFINITION Sequence 99 from Patent WO03048202.

ACCESSION AX775829

VERSION AX775829.1 GI:32693547

KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Matsuda, A. and Muramatsu, S.
TITLE NF-kB activating gene
JOURNAL Patent: WO 03048202-A 99 12-JUN-2003;
Asahi Kasei Kabushiki Kaisha (JP)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

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Searched: 3373863 seqs, 2124099041 residues

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10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2994	78.3	3243	9	AdC37268 Nuclear f
4	2209	57.7	5858	4	AaK80624 Human imm
5	2209	57.7	22893	6	ABK12810 Human tum
6	2037	53.2	5866	4	AaK80625 Human imm
7	2037	53.2	30676	6	ABK12811 Human tum
8	1695	44.3	2246	9	AdC37266 Nuclear f
9	1230	32.1	2207	9	AdC37454 Nuclear f
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22	493	12.9	573	6	ABK12808 Human gen
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C	44	26	0.7	393	7	ABX41090	AbX41090 Bovine ES
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ALIGNMENTS

RESULT 1
ABK12806
ID ABK12806 standard; cDNA; 3826 BP.
AC ABK12806;
XX
XX
DT 18-JUN-2002 (first entry)
XX
DE Human cDNA encoding tumour suppressor CAR-1.
XX
KW Human; ss; tumour suppressor; gene; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer;
KW chromosome ip31-lp36.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 604..2031
FT /tag= a
FT /product= "CAR-1"
FT
XX WO200212285-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
PR 10-AUG-2000; 2000US-0225033P.
PR 23-AUG-2000; 2000US-0227560P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
PI Killary A, Chandler D, Lott S;
XX
DR WPI; 2002-269088/31.
DR P-PSDB; AAU78657.
XX
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
PS Claim 2; Page 134-135; 185pp; English.
XX

CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1, and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence is the cDNA encoding CAR-1
XX
SQ Sequence 3826 BP; 797 A; 1286 C; 999 G; 744 T; 0 U; 0 Other;

Query Match 100.0%; Score 3826; DB 6; Length 3826;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 181 GCTTCTGGCCCTCCCGGACACCGGCCCCACCCCGGGATTTGACCCCCCTTAAGGGCTCCAC 240
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DB 301 CCTCCCGCTCAGGATCTCCGTCCTCTCAGCCGCTCAGAGCTCTCCAGGCGCCATCGCC 360
QY 361 TTGAGTGGCCCACTACCTCTAGACTGCTCCCGGGTGGCGTCCCGAGGAGTCTCAGCC 420
DB 361 TTGAGTGGCCCACTACCTCTAGACTGCTCCCGGGTGGCGTCCCGAGGAGTCTCAGCC 420
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Db 2581 ATGTTCTTACTTCTCCACTGATCTGCTGGTCACTGATGATGCTGTGGCTGTGAAGG 2640

Qy 2641 CACCTGGTAGTGTAGTGCACACATATAGTCAATGTGCCACCACTTCTTSCCCACAGGCC 2700
Db 2641 CACCTGGTAGTGTAGTGCACACATATAGTCAATGTGCCACCACTTCTTSCCCACAGGCC 2700
Qy 2701 GAGGACAGGGTGAAGGTATACCCAAAGCTGATGAGAGCCCATTAGCTTAAAGCAACT 2760
Db 2701 GAGGACAGGGTGAAGGTATACCCAAAGCTGATGAGAGCCCATTAGCTTAAAGCAACT 2760
Qy 2761 GCAGGACAAAGCTCCCTGGATGATCGAGTCCCGAGTCTGTAACAAAGAGTCCAGCCA 2820
Db 2761 GCAGGACAAAGCTCCCTGGATGATCGAGTCCCGAGTCTGTAACAAAGAGTCCAGCCA 2820
Qy 2821 ACCCTCTTACGACAGGCTCTGTGACCTGTAGGCTGAGGAGGCTTCCAGAGCAGTTG 2880
Db 2821 ACCCTCTTACGACAGGCTCTGTGACCTGTAGGCTGAGGAGGCTTCCAGAGCAGTTG 2880
Qy 2881 TTGTAATTTAGGACCCCAAGCACTGGAGGGCTGTGGCTAGACCCCTTGTGACACTTGGC 2940
Db 2881 TTGTAATTTAGGACCCCAAGCACTGGAGGGGCTGTGGCTAGACCCCTTGTGACACTTGGC 2940
Qy 2941 ATCTATCTCAGTTAGGATCTCTGTCAGAAAACAGAGCCACTTGTAGACCCCTTGTGACACTTGGC 2940
Db 2941 ATCTATCTCAGTTAGGATCTCTGTCAGAAAACAGAGCCACTTGTAGCTGTTTAAATTA 3000
Qy 3001 GACAAAGATTTACTACCTGGCCCTGTGGCTTGCAAAATTTGTTGAAAGAGCTGGAGAAG 3060
Db 3001 GACAAAGATTTACTACCTGGCCCTGTGGCTTGCAAAATTTGTTGAAAGAGCTGGAGAAG 3060
Qy 3061 CAGACTCTGCTGAATTTCCAGGAATCCAGGAACTCCAGGCGCAGATTCATCATGTCTGTGTGACCA 3120
Db 3061 CAGACTCTGCTGAATTTCCAGGAATCCAGGAACTCCAGGCGCAGATTCATCATGTCTGTGTGACCA 3120
Qy 3121 GGAAGAGTGGCCCATCTGCAAGAAAGCACTATGTCAGAAAAGCTGCTGACTGCAAGACTA 3180
Db 3121 GGAAGAGTGGCCCATCTGCAAGAAAGCACTATGTCAGAAAAGCTGCTGACTGCAAGACTA 3180
Qy 3181 GGCTCCCTCTGCGCAAGGCTGCGCAAGAAATGTCATTTCCCTAGAAAGAACTTA 3240
Db 3181 GGCTCCCTCTGCGCAAGGCTGCGCAAGAAATGTCATTTCCCTAGAAAGAACTTA 3240
Qy 3241 CTTCACTCAGTTCCTCAATCTTAAATTTTACAGAGATTCCTGTTTGGGGAACCTTAAGTC 3300
Db 3241 CTTCACTCAGTTCCTCAATCTTAAATTTTACAGAGATTCCTGTTTGGGGAACCTTAAGTC 3300
Qy 3301 AGATCCAGAACTTTGGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGAAAGAACTTA 3360
Db 3301 AGATCCAGAACTTTGGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGAAAGAACTTA 3360
Qy 3361 GGTTGGGTGAGCAAGCCCACTGCGTTTTTTCTGCCACAGCATCCAAATCGTGAAGAACT 3420
Db 3361 GGTTGGGTGAGCAAGCCCACTGCGTTTTTTCTGCCACAGCATCCAAATCGTGAAGAACT 3420
Qy 3421 CGGAGAGGGTGGAGTCCACATCTAGGTTGTCTGCGCCCTGGCTCTATCCCTGCCCGAG 3480
Db 3421 CGGAGAGGGTGGAGTCCACATCTAGGTTGTCTGCGCCCTGGCTCTATCCCTGCCCGAG 3480
Qy 3481 AGTTGGGAACTGAGGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCCCGGCTTGCAT 3540
Db 3481 AGTTGGGAACTGAGGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCCCGGCTTGCAT 3540
Qy 3541 TTTCTTTCTAGTCTGGGCTTAGATCTGCACTTGGGCTCTGACACAAACACACCATC 3600
Db 3541 TTTCTTTCTAGTCTGGGCTTAGATCTGCACTTGGGCTCTGACACAAACACACCATC 3600
Qy 3601 CCAAGTAGCCGGAAGAGCTTAAACAGAGGGGTCTTAAATGGTCCCGCCCGCACCCG 3660
Db 3601 CCAAGTAGCCGGAAGAGCTTAAACAGAGGGGTCTTAAATGGTCCCGCCCGCACCCG 3660
Qy 3661 GGCCTCCCTTGGGCAAAAGAAATTTGTCAGCCCTTACCCCAACCCCTTCACTTACAGAACTCT 3720
Db 3661 GGCCTCCCTTGGGCAAAAGAAATTTGTCAGCCCTTACCCCAACCCCTTCACTTACAGAACTCT 3720

QY	1390	AACCTCACATATGAAGACTTCCCGAGCTTCCAAAGTACACAGGCCCCCTGCACTACACCATC	1441
DB	1021	AACCTCACATATGAAGACTTCCCGAGCTTCCAAAGTACACAGGCCCCCTGCACTACACCATC	1080
QY	1450	TGGAAGTCCCTGTTCCAGAGACATCCACCAGTGCAGCGGCCCTTAAACCTTGGACCCGGGC	1509
DB	1081	TGGAAGTCCCTGTTCCAGAGACATCCACCAGTGCAGCGGCCCTTAAACCTTGGACCCGGGC	1140
QY	1510	ACAGCCCAACGAGCCTGATCCTGTGAGACACTGCACATGTGTGGTATTACGGCAACTTG	1569
DB	1141	ACAGCCCAACGAGCCTGATCCTGTGAGACACTGCACATGTGTGGTATTACGGCAACTTG	1200
QY	1570	CACCCACAGCCACTGCAGGACTCGCCTAAAGCGCTTCGATGTGGAGGTGTCCGTGCTGGGT	1629
DB	1201	CACCCACAGCCACTGCAGGACTCGCCTAAAGCGCTTCGATGTGGAGGTGTCCGTGCTGGGT	1260
QY	1630	TCTGAAGCCTTCAGTAGTGGGTCCACTACCTGCGAGGTGTGTGGCGGAGAGACCCAG	1689
DB	1261	TCTGAAGCCTTCAGTAGTGGGTCCACTACCTGCGAGGTGTGTGGCGGAGAGACCCAG	1320
QY	1690	TGGGTGATCGGCTGGCACAGAAAGCGCGCAAGCGCGAGCCGCAAGGCGAGCATCCAGATCCAGCCC	1749
DB	1321	TGGGTGATCGGCTGGCACAGAAAGCGCGAGCCGCAAGGCGAGCATCCAGATCCAGCCC	1380
QY	1750	AGCCCGCGCTTCTACTGATCGTGATGACGATGGCAACAGTACAGCGCTTCACCGAG	1809
DB	1381	AGCCCGCGCTTCTACTGATCGTGATGACGATGGCAACAGTACAGCGCTTCACCGAG	1440
QY	1810	CCCTGGAGCGGGCTTAACGTCGGGACAGACTTCACAAGTGGGTGTCTTCCTGGACTAT	1869
DB	1441	CCCTGGAGCGGGCTTAACGTCGGGACAGACTTCACAAGTGGGTGTCTTCCTGGACTAT	1500
QY	1870	GACCAAGCTTGCTCATCTTCTCAATGCTGATGACATGTCCTGGCTCTACACCTTCCGC	1929
DB	1501	GACCAAGCTTGCTCATCTTCTCAATGCTGATGACATGTCCTGGCTCTACACCTTCCGC	1560
QY	1930	GAGAAGTTCCTGGCAAGCTGTGCTTTACTTCAGCCCTGGCCAGAGCACCAGCAATGCC	1989
DB	1561	GAGAAGTTCCTGGCAAGCTGTGCTTTACTTCAGCCCTGGCCAGAGCACCAGCAATGCC	1620
QY	1990	AAGAACTTCAGCGCTGCGGATACACAGTCCGATCTAGTTCAGGCAAGAGAGACC	2049
DB	1621	AAGAACTTCAGCGCTGCGGATACACAGTCCGATCTAGTTCAGGCAAGAGAGACC	1680
QY	2050	ACAACCTTCCTGGGACCACTGCCACCTGCAGAGACCTGCCAGGAAGATAGAAAGACTGG	2109
DB	1681	ACAACCTTCCTGGGACCACTGCCACCTGCAGAGACCTGCCAGGAAGATAGAAAGACTGG	1739
QY	2110	ACTCCAGCCACCGTGGGCACTGAGAGCTCAGGCCAGTGTGTTTACCCTCCAGCTCCAG	2169
DB	1740	ACTCCAGCCACCGTGGGCACTGAGAGCTCAGGCCAGTGTGTTTACCCTCCAGCTCCAG	1799
QY	2170	TCTGTAATATGAGGTTGCATCCCTACTTCCTTAACTCTCTTCAGATCGATGTTCTG	2229
DB	1800	TCTGTAATATGAGGTTGCATCCCTACTTCCTTAACTCTCTTCAGATCGATGTTCTG	1859
QY	2230	TAGCTCTGACTTGTATAGGATACAGCTTTGATCCAAAGATGTGATGGCTTCCTCTCA	2289
DB	1860	TAGCTCTGACTTGTATAGGATACAGCTTTGATCCAAAGATGTGATGGCTTCCTCTCA	1919
QY	2290	GGGCAACCCCTGCCAACCTTATCCCAATCTTTCAGGGCAGGGGACTACTTTCAGT	2349
DB	1920	GGGCAACCCCTGCCAACCTTATCCCAATCTTTCAGGGCAGGGGACTACTTTCAGT	1979
QY	2350	GTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTTCAGAGCATGCCAGTAGTTGGAG	2409
DB	1980	GTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTTCAGAGCATGCCAGTAGTTGGAG	2039
QY	2410	CCGGAAGACACACAGCACCTCTTATGTGCCATGGCCTTAAGACTTACCCCTGACCAAGC	2469
DB	2040	CCGGAAGACACACACACCTCTTATGTGCCATGGCCTTAAGACTTACCCCTGACCAAGC	2099
QY	2470	TAGTGATGGCCATTTTACCTTTGACCCAGTCCACAGTGGTTCACAGGTAGTACTGTGTC	2529

Db 3180 AGTCCTGGGGCTAGATTCTGCACTTGGGGTCTCTGACACACACACATCCCAAGTAG 3239
QY 3610 CCGAAGAGCTAAACACAGAGGGGTTCTTAAATGGCTGCCCGCCACCCCGGGCTCCCT 3669
Db 3240 CCGAAGAGCTAAACACAGAGGGGTTCTTAAATGGCTGCCCGCCACCCCGGGCTCCCT 3299
QY 3670 TGGGCAAAAGGAATTGTGAGCCCTACCCCAACCCCTTCAACTACCAGATCTGGGCCACCC 3729
Db 3300 TGGGCAAAAGGAATTGTGAGCCCTACCCCAACCCCTTCAACTACCAGATCTGGGCCACCC 3359
QY 3730 CAGCAGTATTTTATTTAAATGTGCCCATTATGATGATGATGATGATGATGATGATGAT 3789
Db 3360 CAGCAGTATTTTATTTAAATGTGCCCATTATGATGATGATGATGATGATGATGATGAT 3419
QY 3790 TTAAGTTACAGATGTC 3806
Db 3420 TTAAGTTACAGATGTC 3436

RESULT 3
ID ADC37268 standard; DNA; 3243 BP.
XX AC ADC37268;
XX DT
XX DE 18-DEC-2003 (first entry)
XX DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 101.
XX KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-Hiv;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
XX OS Homo sapiens.
XX WO2003048202-A2.
XX PN 12-JUN-2003.
XX PD 03-DEC-2002; 2002WO-JP012644.
XX PF 05-DEC-2001; 2001JP-00368692.
XX PR 05-DEC-2001; 2001US-0335829P.
XX PR 03-OCT-2002; 2002JP-00291302.
XX PR 04-OCT-2002; 2002US-0415769P.
XX PA (ASAH) ASahi KASEI KK.
XX PI Matsuda A, Muramatsu S;
XX PI WPI; 2003-505282/47.
XX DR P-PSDB; ADC37269.
XX PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX PT
XX PS Claim 4; SEQ ID NO 101; 938pp; English.
XX CC The present invention relates to novel proteins and their coding
CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischaemic disorders.
XX SQ Sequence 3243 BP; 715 A; 1023 C; 863 G; 642 T; 0 U; 0 Other;
Query Match 78.3%; Score 2994; DB 9; Length 3243;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 3234; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 571 CCTCGGGCCCCCTCTCTGCTGCCCTCGGGCCATGGCGTCAAGCCTCAAGAGCAGCTG 630
Db 10 CCTCGGGCCCCCTCTCTGCTGCCCTCGGGCCATGGCGTCAAGCCTCAAGAGCAGCTG 69
QY 631 CTGTGCTCCATCTCCCTGAGCATCTACAGAGACCCGGTGAAGCTGGGTGCGAGCACTAC 690
Db 70 CTGTGCTCCATCTCCCTGAGCATCTACAGAGACCCGGTGAAGCTGGGTGCGAGCACTAC 129
QY 691 TTCTGCCCGCCCTGCATCAAGAGCACTGTGGTGGCGAGAGGCGAGGCGCCCGGAC 750
Db 130 TTCTGCCCGCCCTGCATCAAGAGCACTGTGGTGGCGAGAGGCGAGGCGCCCGGAC 189
QY 751 TGCCCCAGTGGCGGCGACGCTTCCGCGAGCCCGCTGGCGCCCGAGCTCAAGCTGGCC 810
Db 190 TGCCCCAGTGGCGGCGACGCTTCCGCGAGCCCGCTGGCGCCCGAGCTCAAGCTGGCC 249
QY 811 AACATCGTGGAGCGCTACAGCTCTCTCCCGTGGAGCGCATCTCAAGCGCGCGCGCC 870
Db 250 AACATCGTGGAGCGCTACAGCTCTCTCCCGTGGAGCGCATCTCAAGCGCGCGCC 309
QY 871 GCGGACCCCTGCCAGCGCGACGAGCTCAAGCTCTTCTGCTCACGAGCCCGCGCTT 930
Db 310 GCGGACCCCTGCCAGCGCGACGAGCTCAAGCTCTTCTGCTCACGAGCCCGCGCTT 369
QY 931 CTCTGCTTCTTCTGCGAGCGCTGCACTGCAAGAGCAGCATCAGTCAACCGGCTCGAC 990
Db 370 CTCTGCTTCTTCTGCGAGCGCTGCACTGCAAGAGCAGCATCAGTCAACCGGCTCGAC 429
QY 991 GAGCGCTTCGAGCGAGCTGAGAGGAGTGAAGGACCAACTTCAGGCGCTTCAAGACAGC 1050
Db 430 GAGCGCTTCGAGCGAGCTGAGAGGAGTGAAGGACCAACTTCAGGCGCTTCAAGACAGC 489
QY 1051 GAGCGGGAACACACCGAAGCGCTGAGCTGCTCAAGCGACAACTGCGGAGAGCAAGTCT 1110
Db 490 GAGCGGGAACACACCGAAGCGCTGAGCTGCTCAAGCGACAACTGCGGAGAGCAAGTCT 549
QY 1111 TCCACCAAGAGCTGCGGAGCCTATCGCGGAGGCGCTTCGAGCGGTGACCGGCTGCTG 1170
Db 550 TCCACCAAGAGCTGCGGAGCCTATCGCGGAGGCGCTTCGAGCGGTGACCGGCTGCTG 609
QY 1171 CGTGAAACCGCAGAGGCCATGTAGAGAGCTGGAGGCGGACACGCGCGCGAGCTGACC 1230
Db 610 CGTGAAACCGCAGAGGCCATGTAGAGAGCTGGAGGCGGACACGCGCGCGAGCTGACC 669
QY 1231 GACATCGAGAGAAAGTCCAGCGCTACGCGACGCTGCGCAAGTTCAGAGAGGAGCC 1290
Db 670 GACATCGAGAGAAAGTCCAGCGCTACGCGACGCTGCGCAAGTTCAGAGAGGAGCC 729
QY 1291 CAGATCCTGAGAGCGGCTGGCTGAAACCGACCGGACACCTTCTTGGCTGGGTGGCC 1350
Db 730 CAGATCCTGAGAGCGGCTGGCTGAAACCGACCGGACACCTTCTTGGCTGGGTGGCC 789
QY 1351 TCATCTGCGAGCGGCTCAAGGGAATAATCCATGAGACCACTCATATGAGACTTC 1410
Db 790 TCATCTGCGAGCGGCTCAAGGGAATAATCCATGAGACCACTCATATGAGACTTC 849
QY 1411 CCGACTTCCAAAGTACAGCGCCCTGAGTACACCATCTGGAAGTCCCTGTTCCAGGAC 1470
Db 850 CCGACTTCCAAAGTACAGCGCCCTGAGTACACCATCTGGAAGTCCCTGTTCCAGGAC 909
QY 1471 ATCCACCGAGTGGCGCGCCCTAAACCTGGAACCGGCGACAGCCACCGAGCGCTGATC 1530
Db 910 ATCCACCGAGTGGCGCGCCCTAAACCTGGAACCGGCGCGACAGCCACCGAGCGCTGATC 969
QY 1531 CTGTGCGAGCACTGACCACTTGGCTTACGGCAACTTGGACCCACAGCCACTGAGGAC 1590
Db 970 CTGTGCGAGCACTGACCACTTGGCTTACGGCAACTTGGACCCACAGCCACTGAGGAC 1029
QY 1591 TCGCCAAAGCGCTTCGATGTGGAGGTGTCGGTGTGGGTCTGGAAGCTTTCAGTAGTGGC 1650
Db 1030 TCGCCAAAGCGCTTCGATGTGGAGGTGTCGGTGTGGGTCTGGAAGCTTTCAGTAGTGGC 1089

QY	1651	GTCCA	CTACTG	GGAGG	TGGTGGT	GGCGAGA	AGACCC	AGTGGG	TGATCG	GGCTG	GCACAC	1711
DB	1090	GTCCA	CTACTG	GGAGG	TGGTGGT	GGCGAGA	AGACCC	AGTGGG	TGATCG	GGCTG	GCACAC	1149
QY	1711	GAAG	CCGAAG	CCGCA	AGGCG	AGCATCC	AGATCC	AGCCAG	CCCGCGG	CTTCTA	CTGCATC	1770
DB	1150	GAAG	CCGAAG	CCGCA	AGGCG	AGCATCC	AGATCC	AGCCAG	CCCGCGG	CTTCTA	CTGCATC	1209
QY	1771	GTGAT	GCAAG	TGGCA	CCAGTAC	AGCGC	CTCG	AGGAG	CCCTCG	AGCGCGG	CTTAA	1830
DB	1210	GTGAT	GCAAG	TGGCA	CCAGTAC	AGCGC	CTCG	AGGAG	CCCTCG	AGCGCGG	CTTAA	1269
QY	1831	CGGA	CAAG	CTTG	CAAGG	TGGGTGTCTT	CTCTG	CACTAT	GACCA	AGGCTT	GTCTAT	1890
DB	1270	CGGA	CAAG	CTTG	CAAGG	TGGGTGTCTT	CTCTG	CACTAT	GACCA	AGGCTT	GTCTAT	1329
QY	1891	TACAA	TGCTGA	TGATG	CTGCTG	CTCTAC	ACCTTCC	CGGAG	AGTTCC	CTTGG	CAAGCTC	1950
DB	1330	TACAA	TGCTGA	TGATG	CTGCTG	CTCTAC	ACCTTCC	CGGAG	AGTTCC	CTTGG	CAAGCTC	1389
QY	1951	TGCT	CTTACTT	CAG	CCCTGG	CCAG	CCACG	CCAA	TGGCA	AGACGTT	CAG	2010
DB	1390	TGCT	CTTACTT	CAG	CCCTGG	CCAG	CCACG	CCAA	TGGCA	AGACGTT	CAG	1449
QY	2011	ATCA	ACAC	CCGTCC	GCATCT	AGTCAG	AGCA	AGGAG	ACCA	CAAC	CTTCTG	2070
DB	1450	ATCA	ACAC	CCGTCC	GCATCT	AGTCAG	AGCA	AGGAG	ACCA	CAAC	CTTCTG	1509
QY	2071	CAC	CTGCA	AGAG	CCCTGCC	AGGA	AGATGA	AGAC	CTTGG	ACTCC	AGCCCA	2130
DB	1510	CAC	CTGCA	AGAG	CCCTGCC	AGG	-AGAT	GA	AGAC	CTTGG	ACTCC	1568
QY	2131	TGG	AGAC	CTCAG	GCAG	TGCTTT	TAC	CCCTC	CAG	CCCTC	CA	2190
DB	1569	TGG	AGAC	CTCAG	GCAG	TGCTTT	TAC	CCCTC	CAG	CCCTC	CA	1628
QY	2191	TCC	CTACT	CTCT	AAAC	CTCTCT	C	CAG	CAT	CGATG	TTCTG	2250
DB	1629	TCC	CTACT	CTCT	AAAC	CTCTCT	C	CAG	CAT	CGATG	TTCTG	1688
QY	2251	TAC	AGCTTT	GAT	CCAA	GGATGT	GAC	ATG	GTG	CTTCTC	T	2310
DB	1689	TAC	AGCTTT	GAT	CCAA	GGATGT	GAC	ATG	GTG	CTTCTC	T	1748
QY	2311	CAT	CCCAT	CTCT	C	AGG	GAC	GGAC	TAC	CTTCC	AGTGTCT	2370
DB	1749	CAT	CCCAT	CTCT	C	AGG	GAC	GGAC	TAC	CTTCC	AGTGTCT	1808
QY	2371	GAC	CTCAG	GAAG	TGT	CAG	AGC	ATGG	CGCAG	TAGT	TGG	2430
DB	1809	GAC	CTCAG	GAAG	TGT	CAG	AGC	ATGG	CGCAG	TAGT	TGG	1867
QY	2431	TCT	TATG	TCC	ATG	GGC	CTTA	AGCTTA	CCCTG	ACCA	AGCTAG	2490
DB	1868	TCT	TATG	TCC	ATG	GGC	CTTA	AGCTTA	CCCTG	ACCA	AGCTAG	1927
QY	2491	TGAC	CCCA	GTGCC	ACAG	TGTCA	CAG	AGT	GTACT	CTGT	CT	2550
DB	1928	TGAC	CCCA	GTGCC	ACAG	TGTCA	CAG	AGT	GTACT	CTGT	CT	1987
QY	2551	CT	CTCTG	CCAC	CCCC	CAC	ACCA	CAACT	ATG	GGTTCT	CT	2610
DB	1988	CT	CTCTG	CCAC	CCCC	CAC	ACCA	CAACT	ATG	GGTTCT	CT	2047
QY	2611	GT	CAG	TGAT	GATG	CTGTG	GC	CTGT	GGA	AGCA	CTTGT	2670
DB	2048	GT	CAG	TGAT	GATG	CTGTG	GC	CTGT	GGA	AGCA	CTTGT	2107
QY	2671	CAT	G	TGCC	CA	CACTT	CT	CGCC	CA	GAGG	CGAGG	2730
DB	2108	CAT	G	TGCC	CA	CACTT	CT	CGCC	CA	GAGG	CGAGG	2167

QY	2731	GATGAGAGCCCATTTAGCCTAAAGCAACTCGAGACAAGCCTCCCTGGATGATCGAGGT	2790
Db	2168	GATGCAGAGCCCATTTAGCCTAAAGCAACTCGAGACAAGCCTCCCTGGATGATCGAGGT	2227
QY	2791	CCCCAGTAGCTCTGAACAGAGTCCAGCCAACCCTCTTCAGCAGGCCCTGTGTGACCTGC	2850
Db	2228	CCCCAGTAGCTCTGAACAGAGTCCAGCCAACCCTCTTCAGCAGGCCCTGTGTGACCTGC	2287
QY	2851	TAGGGTGAGGAGGCTCCAGAAGCAGTGTGTATAATTAGSACCAAGCACTGGGAGGGG	2910
Db	2288	TAGGGTGAGGAGGCTCCAGAGAGTGTGTATAATTAGSACCAAGCACTGGGAGGGG	2347
QY	2911	CTGTTGGCTAGACCCCTTGTTCAGACTTGGCATCTATCTCAGTTAGSATCCTGCTGCAGAA	2970
Db	2348	CTGTTGGCTAGACCCCTTGTTCAGACTTGGCATCTATCTCAGTTAGSATCCTGCTGCAGAA	2407
QY	2971	AACAGAGCCACTTGTAGCTGGTTTTAATTAGACAGGATTTATCTGCGGCCCTCGTGG	3030
Db	2408	AACAGAGCCACTTGTAGCTGGTTTTAATTAGACAGGATTTATCTGCGGCCCTCGTGG	2467
QY	3031	CTTGCAAAATTTGTTGGAAGAGCTCGAGAAGCAGACTCTGCTGTAATTTCCAGGAACCTCCA	3090
Db	2468	CTTGCAAAATTTGTTGGAAGAGCTCGAGAAGCAGACTCTGCTGTAATTTCCAGGAACCTCCA	2527
QY	3091	GGCCAGATTCATCATCTGTTGTGACAGGAAGCTGCCCCATCTGCAGGAAGCCAC	3150
Db	2528	GGCCAGATTCATCATCTGTTGTGACAGGAAGCTGCCCCATCTGCAGGAAGCCAC	2587
QY	3151	TATGCCAGAAAGCTGCTGACTGCAGAACCTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCA	3210
Db	2588	TATGCCAGAAAGCTGCTGACTGCAGAACCTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCA	2647
QY	3211	ATAGATGTCTGAGCGCTGCCCTCTCCCACCTTCACCTCAGTCCCAAATCTAAATTTTATA	3270
Db	2648	ATAGATGTCTGAGCGCTGCCCTCTCCCACCTTCACCTCAGTCCCAAATCTAAATTTTATA	2707
QY	3271	CAAGAGATTCCTGTTTGGGGAACTTAAGTCAGATCCAGAACCTTGGCTGCAGGGAGTCT	3330
Db	2708	CAAGAGATTCCTGTTTGGGGAACTTAAGTCAGATCCAGAACCTTGGCTGCAGGGAGTCT	2767
QY	3331	GGGAAATGTCATTTCCCTAGAGGAAGTTAGGTGGGTGGAGCAAGCCCCACCTCGCTTT	3390
Db	2768	GGGAAATGTCATTTCCCTAGAGGAAGTTAGGTGGGTGGAGCAAGCCCCACCTCGCTTT	2827
QY	3391	TTCTGCCACAGCATCCAATCGTCAGAGAACTCGGGAGAGGTGGAGTCCACATCTAGGTT	3450
Db	2828	TTCTGCCACAGCATCCAATCGTCAGAGAACTCGGGAGAGGTGGAGTCCACATCTAGGTT	2887
QY	3451	GTCTGCCCCCTTGGCTCTATCCCTGCCAGAGGTGGAACTCGAGAGTGGCTGCAAGA	3510
Db	2888	GTCTGCCCCCTTGGCTCTATCCCTGCCAGAGGTGGAACTCGAGAGTGGCTGCAAGA	2947
QY	3511	CTGAGCCTAAATGTCTCCCGGCCCTTGACTTTTCTTTCTAGTCTCTGGGCTTAGATTCTG	3570
Db	2948	CTGAGCCTAAATGTCTCCCGGCCCTTGACTTTTCTTTCTAGTCTCTGGGCTTAGATTCTG	3007
QY	3571	CAC TTGGGGTCTCTGACAAACACACATCCCAAAGTACCGGAGAGCTATACACAGGG	3630
Db	3008	CAC TTGGGGTCTCTGACAAACACACATCCCAAAGTACCGGAGAGCTATACACAGGG	3067
QY	3631	GGTTCTTAAATGGCTGCCCGGCCACCCGGGCTCCCTTGGGCAAAAAGGAATTCGTACG	3690
Db	3068	GGTTCTTAAATGGCTGCCCGGCCACCCGGGCTCCCTTGGGCAAAAAGGAATTCGTACG	3127
QY	3691	CCTACCCCAACCTTCAACTACAGATCTGGGCCACCCAGCAGTATTTTTTATTTAAAA	3750
Db	3128	CCTACCCCAACCTTCAACTACAGATCTGGGCCACCCAGCAGTATTTTTTATTTAAAA	3187
QY	3751	TGTTGCCCATTTTATCAGTTATGATCAATTTGTTATTAATTTAAAGTTACAGATGTC	3806
Db	3188	TGTTGCCCATTTTATCAGTTATGATCAATTTGTTATTAATTTAAAGTTACAGATGTC	3243

RESULT 4	PR	14-SEP-2000;	2000US-0232397P.
AAK80624	PR	14-SEP-2000;	2000US-0232398P.
ID AAK80624 standard; DNA; 5858 BP.	PR	14-SEP-2000;	2000US-0232399P.
XX	PR	14-SEP-2000;	2000US-0232400P.
AC AAK80624;	PR	14-SEP-2000;	2000US-0232401P.
XX	PR	14-SEP-2000;	2000US-0233063P.
DT	PR	14-SEP-2000;	2000US-0233064P.
XX	PR	14-SEP-2000;	2000US-0233065P.
XX	PR	21-SEP-2000;	2000US-0234223P.
DE	PR	21-SEP-2000;	2000US-0234274P.
XX	PR	25-SEP-2000;	2000US-0234997P.
XX	PR	25-SEP-2000;	2000US-0234998P.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	PR	26-SEP-2000;	2000US-0235484P.
KW Cytosolic; gene therapy; vaccine; metastasis; ds.	PR	27-SEP-2000;	2000US-0235834P.
XX	PR	27-SEP-2000;	2000US-0235836P.
OS Homo sapiens.	PR	29-SEP-2000;	2000US-0236327P.
XX	PR	29-SEP-2000;	2000US-0236367P.
PN WO2001571182-A2.	PR	29-SEP-2000;	2000US-0236368P.
XX	PR	29-SEP-2000;	2000US-0236369P.
XX	PR	29-SEP-2000;	2000US-0236370P.
PD	PR	02-OCT-2000;	2000US-0236802P.
XX	PR	02-OCT-2000;	2000US-0237037P.
XX	PR	02-OCT-2000;	2000US-0237038P.
XX	PR	02-OCT-2000;	2000US-0237039P.
PR	PR	02-OCT-2000;	2000US-0237040P.
PR	PR	13-OCT-2000;	2000US-0239935P.
PR	PR	13-OCT-2000;	2000US-0239937P.
PR	PR	20-OCT-2000;	2000US-0240960P.
PR	PR	20-OCT-2000;	2000US-0241221P.
PR	PR	20-OCT-2000;	2000US-0241785P.
PR	PR	20-OCT-2000;	2000US-0241786P.
PR	PR	20-OCT-2000;	2000US-0241787P.
PR	PR	20-OCT-2000;	2000US-0241808P.
PR	PR	20-OCT-2000;	2000US-0241809P.
PR	PR	20-OCT-2000;	2000US-0241828P.
PR	PR	01-NOV-2000;	2000US-0244617P.
PR	PR	08-NOV-2000;	2000US-0246474P.
PR	PR	08-NOV-2000;	2000US-0246475P.
PR	PR	08-NOV-2000;	2000US-0246476P.
PR	PR	08-NOV-2000;	2000US-0246477P.
PR	PR	08-NOV-2000;	2000US-0246478P.
PR	PR	08-NOV-2000;	2000US-0246523P.
PR	PR	08-NOV-2000;	2000US-0246524P.
PR	PR	08-NOV-2000;	2000US-0246525P.
PR	PR	08-NOV-2000;	2000US-0246526P.
PR	PR	08-NOV-2000;	2000US-0246527P.
PR	PR	08-NOV-2000;	2000US-0246528P.
PR	PR	08-NOV-2000;	2000US-0246532P.
PR	PR	08-NOV-2000;	2000US-0246609P.
PR	PR	08-NOV-2000;	2000US-0246610P.
PR	PR	08-NOV-2000;	2000US-0246611P.
PR	PR	08-NOV-2000;	2000US-0246613P.
PR	PR	17-NOV-2000;	2000US-0249207P.
PR	PR	17-NOV-2000;	2000US-0249208P.
PR	PR	17-NOV-2000;	2000US-0249209P.
PR	PR	17-NOV-2000;	2000US-0249210P.
PR	PR	17-NOV-2000;	2000US-0249211P.
PR	PR	17-NOV-2000;	2000US-0249212P.
PR	PR	17-NOV-2000;	2000US-0249213P.
PR	PR	17-NOV-2000;	2000US-0249214P.
PR	PR	17-NOV-2000;	2000US-0249215P.
PR	PR	17-NOV-2000;	2000US-0249216P.
PR	PR	17-NOV-2000;	2000US-0249217P.
PR	PR	17-NOV-2000;	2000US-0249218P.
PR	PR	17-NOV-2000;	2000US-0249244P.
PR	PR	17-NOV-2000;	2000US-0249245P.
PR	PR	17-NOV-2000;	2000US-0249264P.
PR	PR	17-NOV-2000;	2000US-0249265P.
PR	PR	17-NOV-2000;	2000US-0249297P.
PR	PR	17-NOV-2000;	2000US-0249299P.
PR	PR	01-DEC-2000;	2000US-0250160P.
PR	PR	01-DEC-2000;	2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 35436; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 5858 BP; 1455 A; 1579 C; 1490 G; 1334 T; 0 U; 0 Other;
XX
XX
XX Query Match 57.7%; Score 2209; DB 4; Length 5858;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2329; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1478 CAGTGCACGCGCCCTAACCTTGGACCCCGGGCAGCCACAGCCCTGATCCTGTCGG 1537
DB 6 CAGTGCACGCGCCCTAACCTTGGACCCCGGGCAGCCACAGCCCTGATCCTGTCGG 65
QY 1538 ACGACTGCACCATTTGGCTTAGGGCACTTGCACCCAGCCACTGCAGGATCCGCA 1597
DB 66 ACGCTGCACCATTTGGCTTAGGGCACTTGCACCCAGCCACTGCAGGATCCGCA 125
QY 1598 AGCGCTTCGATGTGGAGGTGTGGTCTGCTGGGTCTGAAGCCTTCAGTAGTGGGTCCACT 1657
DB 126 AGCGCTTCGATGTGGAGGTGTGGTCTGCTGGGTCTGAAGCCTTCAGTAGTGGGTCCACT 185
QY 1658 ACTGGAGGTGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCAGCAGAGCCG 1717
DB 186 ACTGGAGGTGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCAGCAGAGCCG 245
QY 1718 CAAGCCGCAAGGCGACATCCAGATCCAGCCAGCCCGCGGCTTCTACTGATCGTATGC 1777
DB 246 CAAGCCGCAAGGCGACATCCAGATCCAGCCAGCCCGCGGCTTCTACTGATCGTATGC 305
QY 1778 ACGATGGCAACAGTACAGCGCTGACAGCGCCCTGGACGGCTTAAAGCTCCGGGACA 1837
DB 306 ACGATGGCAACAGTACAGCGCTGACAGCGCCCTGGACGGCTTAAAGCTCCGGGACA 365
QY 1838 ACGTTGCAAGGTGGGTGTCTTCTGGACTATGACCAAGGCTTGCTTCATCTTCAATG 1897
DB

DB 366 AGCTTGACAAAGTGGGTGTCTTCTTGACATATGACCAAGGTTCTCATCTTCTACAAATG 425
QY 1898 CTGATGACATGTCTCTGGCTCTACACCTTCCGCGAGAAAGTTCCCTGGCAAGCTCTGCTCTTT 1957
DB 426 CTGATGACATGTCTCTGGCTCTACACCTTCCGCGAGAAAGTTCCCTGGCAAGCTCTGCTCTTT 485
QY 1958 ACTTCAGCCCTTGGCCAGAGCAGCCCAATGGCAAGAAAGTTTCAGCCGCTGGGATCAACA 2017
DB 486 ACTTCAGCCCTTGGCCAGAGCAGCCCAATGGCAAGAAAGTTTCAGCCGCTGGGATCAACA 545
QY 2018 CCGTCCGCATCTAGTCCAGGAGAGGAGACCAACCTCTCTGGGACCACTTGCCACCTGC 2077
DB 546 CCGTCCGCATCTAGTCCAGGAGAGGAGACCAACCTCTCTGGGACCACTTGCCACCTGC 605
QY 2078 AAGAGCCCTGCCAGGAAGATAGAAGACCTTGGACTCCAGCCCAACCGTGGCCACTGGAGAC 2137
DB 606 AAGAGCCCTGCCCAGG-AGATAGAAGACCTTGGACTCCAGCCCAACCGTGGCCACTGGAGAC 664
QY 2138 CTGAGGCCAGTCTTTACCCCTCCAGCTCCAGTCTGTAAATGGAGTTGCATTCCTTAC 2197
DB 665 CTGAGGCCAGTCTTTACCCCTCCAGCTCCAGTCTGTAAATGGAGTTGCATTCCTTAC 724
QY 2198 TTCTTAACTCTCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCT 2257
DB 725 TTCTTAACTCTCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCT 784
QY 2258 TTGATCCAGGATGTGACATGGCTTCTCTCAGGCAACCCCTGCCCAACCCCTCATCCCC 2317
DB 785 TTGATCCAGGATGTGACATGGCTTCTCTCAGGCAACCCCTGCCCAACCCCTCATCCCC 844
QY 2318 ATCTTCTCAGGGCAGGGGACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA 2377
DB 845 ATCTTCTCAGGGCAGGGGACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA 904
QY 2378 GGAAGTGTGACGATGGCCAGTAGTTGGCAGCCCGAAGACACACAGCAGCCCTTATG 2437
DB 905 GGAAGTGTGACGATGGCCAGTAGTTGGCAGCCCGAAGACACACAGCAGCCCTTATG 964
QY 2438 TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCTTTGACCCC 2497
DB 965 TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCTTTGACCCC 1024
QY 2498 AGTCCACAGTGTGTCAGGTAGTACCTGCTCTAGGTTGCTCAGAGCCAACTCTCT 2557
DB 1025 AGTCCACAGTGTGTCAGGTAGTACCTGCTCTAGGTTGCTCAGAGCCAACTCTCT 1084
QY 2558 GCCACCCCCACACCAAGAACTATATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2617
DB 1085 GCCACCCCCACACCAAGAACTATATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1144
QY 2618 ATGATGCTGTGGCTGTGGAAGGACCTGTGTAGTTGAGTCCACATTAATAGTCAATGTGC 2677
DB 1145 ATGATGCTGTGGCTGTGGAAGGACCTGTGTAGTTGAGTCCACATTAATAGTCAATGTGC 1204
QY 2678 CACCACTTCTGCCCACAGGCGGAGGAGGATAGGAGTATACCAAGCTGATGCAG 2737
DB 1205 CACCACTTCTGCCCACAGGCGGAGGAGGATAGGAGTATACCAAGCTGATGCAG 1264
QY 2738 AGCCCATTAGCCCTAAAGCAACTGAGGACAAAGCCCTCCCTGGATGATCGAGGTCCCCAGT 2797
DB 1265 AGCCCATTAGCCCTAAAGCAACTGAGGAGCAAGCCCTCCCTGGATGATCGAGGTCCCCAGT 1324
QY 2798 AGCTCTGAACAAGAGTCCAGCCAAACCTTCTTCCAGCCAGCCCTCTGTGACCTGTAGGGTG 2857
DB 1325 AGCTCTGAACAAGAGTCCAGCCAAACCTTCTTCCAGCCAGCCCTCTGTGACCTGTAGGGTG 1384
QY 2858 CAGGAGGCTTCCAGAGCAGTGTGTTGTAATAGGACCCAGCAGCTGGGAGGGGCTGTTGG 2917
DB 1385 CAGGAGGCTTCCAGAGCAGTGTGTTGTAATAGGACCCAGCAGCTGGGAGGGGCTGTTGG 1444
QY 2918 CTAGACCCCTTGTGAGACTTGGCACTTCTCAGTTAGGATCCTGTCAGAAAAACAAGA 2977
DB 1445 CTAGACCCCTTGTGAGACTTGGCACTTCTCAGTTAGGATCCTGTCAGAAAAACAAGA 1504

QY	2978	GCCACCTGTAGCTGGTTTAAATAGACAAGGATTATTAACCTGGCCCTCGTGGCTTCCAA	3037	KW	bacteria artificial chromosome; chromosome lp31-lp36.
Db	1505	GCACCTGTAGCTGGTTTAAATAGACAAGGATTATTAACCTGGCCCTCGTGGCTTCCAA	1564	OS	
QY	3038	AATTGTTGGAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAATCCACGCGCAG	3097	XX	Homo sapiens.
Db	1565	AATTGTTGGAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAATCCACGCGCAG	1624	FT	Key
QY	3098	ATTTCATCATGCTCTGCTGACACAGAAAGCTGCCCCCACTCTGCAGGAAGCCACTATGCCA	3157	FT	misc_feature
Db	1625	ATTTCATCATGCTCTGCTGACACAGAAAGCTGCCCCCACTCTGCAGGAAGCCACTATGCCA	1684	FT	Location/Qualifiers
QY	3158	GAAGCTGCTGACTGCGAGAACTAGGCTCCCTCTGCGCAGCGTCCGTCAGCAATAGATG	3217	EN	5820
Db	1685	GAAGCTGCTGACTGCGAGAACTAGGCTCCCTCTGCGCAGCGTCCGTCAGCAATAGATG	1744	XX	/*tag= a
QY	3218	TCCTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCTCAAAATCTAAATTTTACAAGAGA	3277	XX	/note= "Nucleotides 5821-6360 of the present sequence as reproduced in the specification are illegible or missing, nucleotide 5821 of the present sequence corresponds to nucleotide 6361 of sequence as printed in the specification"
Db	1745	TCCTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCTCAAAATCTAAATTTTACAAGAGA	1804	XX	WO200212285-A2.
QY	3278	TTCTGTTTGGGGAACTTAAGTCAATCCAGAACTTGGCTGCAAGGAGTCTGGGAAAT	3337	XX	14-FEB-2002.
Db	1805	TTCTGTTTGGGGAACTTAAGTCAATCCAGAACTTGGCTGCAAGGAGTCTGGGAAAT	1864	XX	09-AUG-2001; 2001WO-US025269.
QY	3338	GTCAATTTCCCTAGAGAGTAGGTGGTGGAGCAGCCACCTCGGTTTTTCTGCC	3397	XX	10-AUG-2000; 2000US-0225033P.
Db	1865	GTCAATTTCCCTAGAGAGTAGGTGGTGGAGCAGCCACCTCGGTTTTTCTGCC	1924	XX	23-AUG-2000; 2000US-0227560P.
QY	3398	ACAGATCCCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCG	3457	XX	(TEXA) UNIV TEXAS SYSTEM.
Db	1925	ACAGATCCCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCG	1984	XX	Killary A, Chandler D, Lott S;
QY	3458	CCCTTGGCTCTATCCCTGCCAGAGTGGGAACTGGAGAGTGGCTGCAAGACTGAGCC	3517	XX	WPI; 2002-269088/31.
Db	1985	CCCTTGGCTCTATCCCTGCCAGAGTGGGAACTGGAGAGTGGCTGCAAGACTGAGCC	2044	XX	New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for diagnosing cancer, for altering the phenotype of a tumor cell, for treating cancers or as a diagnostic or prognostic indicator of cancer.
QY	3518	TAAATGCTCCCGGCTTGACTTTCTTCTAGTCTGGGCTTGTAGTCTGACCTGG	3577	XX	Disclosure; Page 170-176; 185pp; English.
Db	2045	TAAATGCTCCCGGCTTGACTTTCTTCTAGTCTGGGCTTGTAGTCTGACCTGG	2104	XX	The invention relates to an isolated polynucleotide encoding a polypeptide being tumor suppressor, CAR-1. Also included are fragments of the polynucleotide from 15-5000 nucleotides, fragments of the protein from 10-50 amino acids, an expression cassette comprising the polynucleotide under the control of a promoter operable in eukaryotic cells, a method for suppressing growth of a cancer cells by contacting the cells with the expression cassette (i.e. gene therapy), a cell comprising the expression cassette, an anti-CAR-1 monoclonal or polyclonal antibody, a hybridoma cell that produces the monoclonal antibody, a method of diagnosing a cancer by assessing the expression of CAR-1 tumor suppressor in the cells of a tissue sample from a subject, methods for altering the phenotype of a tumor cell, methods for treating a subject with cancer by administering the tumor suppressor CAR-1 and a promoter active in eukaryotic cells, where the promoter is operably linked to the region encoding the functional CAR-1 gene, a non-human transgenic eukaryote that over-expresses CAR-1 as compared to a similar non-transgenic eukaryote, a method of screening a candidate substance for anti-tumor activity by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance and determining the effect of the candidate substance on the cell, an anti-tumor composition produced by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance, determining the effect of the candidate substance on the cell, identifying a candidate inhibitor substance, and making a composition of an isolated and purified nucleic acid that hybridizes, under high stringency conditions, to a DNA segment comprising about 15-3826 bases of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for altering the phenotype of a tumor cell, for treating cancers (e.g. cancer of the brain, lung, liver, kidney, lymph node, pancreas, small intestine, blood cells, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or other tissues), and as a diagnostic or prognostic indicator of cancer. CAR-1 may also be used in screening compounds for activity in either stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the effect of mutant CAR-1 molecule. The gene for CAR-1 is located on chromosome 1 (lp31-lp36). The present sequence is a BAC (bacterial artificial chromosome) containing part of the CAR-1 gene
QY	3638	AAATGCTGCTCCCGCCACCCGCGCTCCCTTGGGCAAAAGAAATGTCAGCCCTACCC	3697	XX	
Db	2165	AAATGCTGCTCCCGCCACCCGCGCTCCCTTGGGCAAAAGAAATGTCAGCCCTACCC	2224	XX	
QY	3698	CAACCTTCACTACCAATCTGGCCACCCGACGATTTTATTAAATGTTGCC	3757	XX	
Db	2225	CAACCTTCACTACCAATCTGGCCACCCGACGATTTTATTAAATGTTGCC	2284	XX	
QY	3758	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	3807	XX	
Db	2285	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	2334	XX	
QY	3807	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	3870	XX	
Db	2334	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	2387	XX	
QY	3870	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	3927	XX	
Db	2387	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	2444	XX	
QY	3927	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	3987	XX	
Db	2444	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	2500	XX	
QY	3987	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4050	XX	
Db	2500	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4100	XX	
QY	4050	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4150	XX	
Db	4100	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4200	XX	
QY	4150	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4250	XX	
Db	4200	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4300	XX	
QY	4250	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4350	XX	
Db	4300	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4400	XX	
QY	4350	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4450	XX	
Db	4400	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4500	XX	
QY	4450	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4550	XX	
Db	4500	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4600	XX	
QY	4550	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4650	XX	
Db	4600	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4700	XX	
QY	4650	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4750	XX	
Db	4700	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4800	XX	
QY	4750	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4850	XX	
Db	4800	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4900	XX	
QY	4850	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	4950	XX	
Db	4900	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5000	XX	
QY	4950	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5050	XX	
Db	5000	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5100	XX	
QY	5050	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5150	XX	
Db	5100	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5200	XX	
QY	5150	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5250	XX	
Db	5200	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5300	XX	
QY	5250	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5350	XX	
Db	5300	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5400	XX	
QY	5350	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5450	XX	
Db	5400	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5500	XX	
QY	5450	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5550	XX	
Db	5500	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5600	XX	
QY	5550	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5650	XX	
Db	5600	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5700	XX	
QY	5650	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5750	XX	
Db	5700	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5800	XX	
QY	5750	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5850	XX	
Db	5800	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5900	XX	
QY	5850	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	5950	XX	
Db	5900	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6000	XX	
QY	5950	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6050	XX	
Db	6000	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6100	XX	
QY	6050	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6150	XX	
Db	6100	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6200	XX	
QY	6150	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6250	XX	
Db	6200	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6300	XX	
QY	6250	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6350	XX	
Db	6300	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6400	XX	
QY	6350	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6450	XX	
Db	6400	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6500	XX	
QY	6450	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6550	XX	
Db	6500	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6600	XX	
QY	6550	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6650	XX	
Db	6600	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6700	XX	
QY	6650	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6750	XX	
Db	6700	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6800	XX	
QY	6750	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6850	XX	
Db	6800	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6900	XX	
QY	6850	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	6950	XX	
Db	6900	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7000	XX	
QY	6950	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7050	XX	
Db	7000	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7100	XX	
QY	7050	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7150	XX	
Db	7100	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7200	XX	
QY	7150	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7250	XX	
Db	7200	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7300	XX	
QY	7250	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7350	XX	
Db	7300	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7400	XX	
QY	7350	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7450	XX	
Db	7400	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7500	XX	
QY	7450	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7550	XX	
Db	7500	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7600	XX	
QY	7550	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7650	XX	
Db	7600	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7700	XX	
QY	7650	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7750	XX	
Db	7700	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7800	XX	
QY	7750	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7850	XX	
Db	7800	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7900	XX	
QY	7850	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	7950	XX	
Db	7900	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8000	XX	
QY	7950	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8050	XX	
Db	8000	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8100	XX	
QY	8050	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8150	XX	
Db	8100	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8200	XX	
QY	8150	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8250	XX	
Db	8200	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8300	XX	
QY	8250	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8350	XX	
Db	8300	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8400	XX	
QY	8350	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8450	XX	
Db	8400	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8500	XX	
QY	8450	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8550	XX	
Db	8500	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8600	XX	
QY	8550	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8650	XX	
Db	8600	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8700	XX	
QY	8650	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8750	XX	
Db	8700	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8800	XX	
QY	8750	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8850	XX	
Db	8800	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8900	XX	
QY	8850	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	8950	XX	
Db	8900	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9000	XX	
QY	8950	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9050	XX	
Db	9000	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9100	XX	
QY	9050	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9150	XX	
Db	9100	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9200	XX	
QY	9150	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9250	XX	
Db	9200	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9300	XX	
QY	9250	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9350	XX	
Db	9300	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9400	XX	
QY	9350	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9450	XX	
Db	9400	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9500	XX	
QY	9450	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9550	XX	
Db	9500	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9600	XX	
QY	9550	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9650	XX	
Db	9600	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9700	XX	
QY	9650	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9750	XX	
Db	9700	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9800	XX	
QY	9750	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9850	XX	
Db	9800	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9900	XX	
QY	9850	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	9950	XX	
Db	9900	CATTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA	10000	XX	

SQ	Sequence	22893 BP; 5720 A; 5989 C; 5664 G; 5415 T; 0 U; 105 Other;
	Query Match	57.7%; Score 2209; DB 6; Length 22893;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2329; Conservative	0; Mismatches 0; Indels 1; Gaps 1;
QY	1478	CAGTGGCAGCGCCCTAAACCTGACCGCGGCACAGCCACAGCCACGAGCGCTGATCCTGTCGG 1537
DB	11989	CAGTGGCAGCGCCCTAAACCTGACCGCGGCACAGCCACGAGCGCTGATCCTGTCGG 12048
QY	1538	ACGACTGCACCATGTGGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAA 1597
DB	12049	ACGACTGCACCATGTGGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAA 12108
QY	1598	AGCGCTTCGATGTGGAGGTGCGTGTGGTTCCTGAAGCCTTCAGTAGTGGGTCCACT 1657
DB	12109	AGCGCTTCGATGTGGAGGTGCGTGTGGTTCCTGAAGCCTTCAGTAGTGGGTCCACT 12168
QY	1658	ACTGGGAGGTGGTGGCGGAGAGAACCCAGTGGGTGATCGGGCTGGCACACGAGCCG 1717
DB	12169	ACTGGGAGGTGGTGGCGGAGAGAACCCAGTGGGTGATCGGGCTGGCACACGAGCCG 12228
QY	1718	CAAGCCGAAGGGCAGCATCCAGATCCAGCCCGCCGCGCTTCTACTGATCGTGATGC 1777
DB	12229	CAAGCCGAAGGGCAGCATCCAGATCCAGCCCGCCGCGCTTCTACTGATCGTGATGC 12288
QY	1778	ACGATGCAACCAAGTACAGCGCTGCACGAGCGCTTGACCGGCTTAAAGTTCGGGACA 1837
DB	12289	ACGATGCAACCAAGTACAGCGCTGCACGAGCGCTTGACCGGCTTAAAGTTCGGGACA 12348
QY	1838	AGCTTGACAGGTGGGTGTCTTCTGTGACTATGACCAAGGCTTGCTCATCTTCTACAATG 1897
DB	12349	AGCTTGACAGGTGGGTGTCTTCTGTGACTATGACCAAGGCTTGCTCATCTTCTACAATG 12408
QY	1898	CTGATGACATGTCTCTGGCTCTACACTTCCGAGAGATTGCCCTGGCAAGCTCTGCTCTT 1957
DB	12409	CTGATGACATGTCTCTGGCTCTACACTTCCGAGAGATTGCCCTGGCAAGCTCTGCTCTT 12468
QY	1958	ACTTACGCGCTGSCCAGAGCCAGCCAAATGGCAAGACGTTTCAGCCGCTGCGGATCAACA 2017
DB	12469	ACTTACGCGCTGSCCAGAGCCAGCCAAATGGCAAGACGTTTCAGCCGCTGCGGATCAACA 12528
QY	2018	CGTCCGCACTTAGTCCAGGAGAGACCAACAACCTCTCGGACCACTGCCACTGC 2077
DB	12529	CGTCCGCACTTAGTCCAGGAGAGAGACCAACAACCTCTCGGACCACTGCCACTGC 12588
QY	2078	AAGAGCCCTGCCAGGAAGATAGAGACTTGGACTCCAGCCCAACCGTGGCCACTGGAGAC 2137
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QY	2138	CTCAGGCCAGTTGTTTACCTCCAGCTCCAGCTCCAGTCTGTAATGGAGGTTGCAATCCCTAC 2197
DB	12648	CTCAGGCCAGTTGTTTACCTCCAGCTCCAGCTCCAGTCTGTAATGGAGGTTGCAATCCCTAC 12707
QY	2198	TTCTTAACTCTCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCT 2257
DB	12708	TTCTTAACTCTCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCT 12767
QY	2258	TTGATCCAGGATGTGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCCCTCATCCCC 2317
DB	12769	TTGATCCAGGATGTGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCCCTCATCCCC 12827
QY	2318	ATCTTCTCAGGGGCAAGGACTACCTTCCAGTGTCTCTCCCTCCAGCCCAAGCCCTGACCTCA 2377
DB	12828	ATCTTCTCAGGGGCAAGGACTACCTTCCAGTGTCTCTCCCTCCAGCCCAAGCCCTGACCTCA 12887
QY	2378	GGAAGTGTACAGACATGGCCAGTAGTTGGAGCCCGAAAGACACACAGACCCCTCTTATG 2437
DB	12888	GGAAGTGTACAGACATGGCCAGTAGTTGGAGCCCGAAAGACACACAGACCCCTCTTATG 12947
QY	2438	TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTAGTGGGCCAATTACCTTGAACCC 2497
DB	12948	TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTAGTGGGCCAATTACCTTGAACCC 13007
QY	2498	AGTCCACAGTGGTACACAGGTAGTACCTGGTCTAGGGTGTGCTGAGAGCCAAACCTCTCCT 2557
DB	13008	AGTCCACAGTGGTACACAGGTAGTACCTGGTCTAGGGTGTGCTGAGAGCCAAACCTCTCCT 13067
QY	2558	GCCACCCCCACACCAAGAACTATATGTTCTTACTTCTCCACATGATCTGCTGTGTCAGTG 2617
DB	13068	GCCACCCCCACACCAAGAACTATATGTTCTTACTTCTCCACATGATCTGCTGTGTCAGTG 13127
QY	2618	ATGATGCTGTGGCTGTGGAAGCACCTGTGTAGTTAGTCCACATATATAGTCAATGTGC 2677
DB	13128	ATGATGCTGTGGCTGTGGAAGCACCTGTGTAGTTAGTCCACATATATAGTCAATGTGC 13187
QY	2678	CACACCTTCTCCACACAGCCGAGGACAGGGTGAAGGTATACCCAAAGCTCATGCAG 2737
DB	13188	CACACCTTCTCCACACAGCCGAGGACAGGGTGAAGGTATACCCAAAGCTCATGCAG 13247
QY	2738	AGCCCATTAGCCTTAAAGCAACTGACGCAAGCTCCCTGGATGATCGAGGTCCCCAGT 2797
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QY	2798	AGCTCTGAAACAAGTCCAGCCAAACCTCTTACGCCAGGCTCTGTGACCTGTGAGGCTG 2857
DB	13308	AGCTCTGAAACAAGTCCAGCCAAACCTCTTACGCCAGGCTCTGTGACCTGTGAGGCTG 13367
QY	2858	CAGAGGCTTCCAGAGCAAGTGTGTGTAATTAGGACCCAGACACTGGGAGGGGCTGTGCG 2917
DB	13368	CAGAGGCTTCCAGAGCAAGTGTGTGTAATTAGGACCCAGACACTGGGAGGGGCTGTGCG 13427
QY	2918	CTAGACCCCTGTCAGACTTGGCATCTATCTCAGTTAGGATCTCTGTGCAAGAAAACAGA 2977
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QY	3038	AATTGTGGAAGAGCTGGAGAGACACTCTGCTGAATTTCCAGGAACCTCCACAGCCAG 3097
DB	13548	AATTGTGGAAGAGCTGGAGAGACACTCTGCTGAATTTCCAGGAACCTCCACAGCCAG 13607
QY	3098	ATTTCATGATGCTGTGTGTCACAGGAAGCTGCCCCATCTGCAGGAAGCCATATGCCA 3157
DB	13608	ATTTCATGATGCTGTGTGTCACAGGAAGCTGCCCCATCTGCAGGAAGCCATATGCCA 13667
QY	3158	GAAAGCTGTGACTGCAGAACTAGGCTCCCTCTGCCCACGGTCCGTGCCAGCCAAATAGATG 3217
DB	13668	GAAAGCTGTGACTGCAGAACTAGGCTCCCTCTGCCCACGGTCCGTGCCAGCCAAATAGATG 13727
QY	3218	TCTGAGGCTGCCCTCTTCCCACTTCACTCAGTTCCCAAACTTAAATTTTACAAGAGA 3277
DB	13728	TCTGAGGCTGCCCTCTTCCCACTTCACTCAGTTCCCAAACTTAAATTTTACAAGAGA 13787
QY	3278	TTCTGTTTGGGGGAACTTAAAGTCAGATCCAGAACCTTGCTGCTCAAGGGAGTCTGGAAAT 3337
DB	13788	TTCTGTTTGGGGGAACTTAAAGTCAGATCCAGAACCTTGCTGCTCAAGGGAGTCTGGAAAT 13847
QY	3338	GTCAATTTCCCTAGAAGGAGTTAGGGTGGGTGAGCAAGCCCACTGCTGCTTTTCTGCC 3397
DB	13848	GTCAATTTCCCTAGAAGGAGTTAGGGTGGGTGAGCAAGCCCACTGCTGCTTTTCTGCC 13907
QY	3398	ACAGCATCCATCTGTAGAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGGTGTCTCTGC 3457
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QY	3458	CCCTTGGCTCTATCCCTGCCAGAGGTGGAACTCGAGAGTGGGCTGCAAGACTGAGCC 3517
DB	13968	CCCTTGGCTCTATCCCTGCCAGAGGTGGAACTCGAGAGTGGGCTGCAAGACTGAGCC 14027
QY	3518	TAAATGTCTCCCGGCTTGAATTTCTTTCTAGTCTGGGCTTAGATTTCTGCACTTGG 3577
DB	14028	TAAATGTCTCCCGGCTTGAATTTCTTTCTAGTCTGGGCTTAGATTTCTGCACTTGG 14087

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QY 3578 GGTCTCTGACAAACACACATCCCAAAGTAGCCGAGAGCTAAACACAGGGGGTTCCT 3637
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QY 3638 AAAATGCTGCTCCCGCCACCCGGGCTCCCTTTGGGCAAAAGGAATGTGAGCCCTACCC 3697
DB 14148 AAAATGCTGCTCCCGCCACCCGGGCTCCCTTTGGGCAAAAGGAATGTGAGCCCTACCC 14207
QY 3698 CAACCCCTTCAACTACCAAGATCTGGGCCACCCAGCAGTATTTTAAATTTAAATGTTGCC 3757
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DT 07-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35437.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
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XX WO200157182-A2.
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XX 09-AUG-2001.
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XX 17-JAN-2001; 2001WO-US001354.
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Qy	2798	AGCTCTGAACAAGATCCAGC	CAACCCCTCTTCAGCCAGG	CCCTCTGTGACCTGCTAGGGTG	2857
Db	1324	AGCTCTGAACAAGATCCAGC	CAACCCCTCTTCAGCCAGG	CCCTCTGTGACCTGCTAGGGTG	1383
Qy	2858	CAGGAGCCTTCCAGAAGCAG	TGTGTTGTAATTAGGACCC	CAAGCACTGGGAGGGGCTGTGG	2917
Db	1384	CAGGAGCCTTCCAGAAGCAG	TGTGTTGTAATTAGGACCC	CAAGCACTGGGAGGGGCTGTGG	1443
Qy	2918	CTAGACCCCTTGTCAGACT	TGGCATCTATCTCAGTTAG	GATCCTGCTGCAGAAAAACA	2977
Db	1444	CTGACCCCTTGTCAGACT	TGGCATCTATCTCAGTTAG	GATCCTGCTGCAGAAAAACA	1503
Qy	2978	GCACATGTAGCTGGTTTA	ATTAGACAAGGATTTACT	ACTGGCCCCCTGGTGGCTGCAA	3033
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Qy	3038	AAATTGTTGGAGAGCTGG	AAGACAGACTCTGTGAAT	TTCCAGGAACCTCCAGGCCAG	3097
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Qy	3098	ATTCAATCATGCTGTTGT	GCACAGGAAGCTGCCCAT	CTGCAGGAAGCCATATGCCA	3157
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Qy	3158	GAAGCTGCTCACTGCA	GAACCTAGGCTCCCTCT	GCACAGGCTCCGTCAGCCAAATAGATG	3217
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Qy	3218	TCCTGAGGCCTGCCCT	CTCCCATCTCACTAGT	TCCCAATCTAAATTTTACAGAGA	3277
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Qy	3278	TTCTGTTTGGGGAACT	TAAGTCAAGTCCAGAA	CCCTTGGCTGCAAGGGAGCTCGCGAAAT	3337
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Qy	3338	GTCACTTCCCTAGAGGA	AGTTAGGGTGGGTGG	AGCAAGCCCCACCTGCGTTTCTGCC	3397
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Qy	3578	GGTCTCTGACAACA	CAACATCCCAAGTAC	CGGAGAGCTTAACACAGGGGTTCTT	3637
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Qy	3638	AAATGGCTGCCCGCC	CCAGCCCGGCTCCCT	TGGGCAAAAGGAATTTGTCAGCCCTACCC	3697
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Qy	3698	CAAGCCCTCAACTAC	CAGAACTCTGGGCC	CAACCCAGCAGTATTTTATTTAAATGTTGCC	3757
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Qy	3758	CATTTTATGAGTTAT	GATCAATTTGTTTAA	ATAAGTTACAGATGTCA	3807
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RESULT 7

ABK12811

ABK12811
TD ABK12811 standard; DNA; 30676 BP.

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ID AB12011

AC ABK12811;

AC
XX
ADTCTT /

DT 18-JUN-2002 (first entry)

XX Human tumour suppressor CAR-1, BAC clone RP11-131M11.
DE
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XX Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW herpesvirus-thymidine kinase; human chromosome 1p36.
KW herpesvirus-thymidine kinase; human chromosome 1p36.

KW bacteria art
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Homo sapiens.

OS Homo sapiens
yy

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WO200212285-A2.

PN MOZ00Z12Z283-A42.
XX

XX PD 14-FEB-2002.

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09-AUG-2001; 2001WO-US025269.

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PR 23-AUG-2000; 2000US-0227560P.
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XX (TEXA) UNIV TEXAS SYSTEM.
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PI Killary A, Chandler D, Lott S;
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XX WPI; 2002-269088/31.
XX
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT detecting a metastatic or premetastatic indicator of cancer.

PT treating cancers or as a diagnostic or pr

Disclosure; Page 176-185; 185pp; English.

The invention relates to an isolated polynucleotide encoding a polypeptide being tumour suppressor, CAR-1. Also included are fragments of the polynucleotide from 15-5000 nucleotides, fragments of the protein from 10-50 amino acids, an expression cassette comprising the polynucleotide under the control of a promoter operable in eukaryotic cells, a method for suppressing growth of a cancer cells by contacting the cells with the expression cassette (i.e. gene therapy), a cell comprising the expression cassette, an anti-CAR-1 monoclonal or polyclonal antibody, a hybridoma cell that produces the monoclonal antibody, a method of diagnosing a cancer by assessing the expression of CAR-1 tumour suppressor in the cells of a tissue sample from a subject, methods for altering the phenotype of a tumour cell, methods for treating a subject with cancer by administering the tumour suppressor CAR-1, or by administering a nucleic acid encoding the tumour suppressor CAR-1, or by promoter active in eukaryotic cells, where the promoter is operably linked to the region encoding the tumour suppressor, a non-human transgenic eukaryote lacking a functional CAR-1 gene, a non-human transgenic eukaryote that over-expresses CAR-1 as a candidate substance for non-transgenic eukaryote, a method of screening a cell lacking functional CAR-1 anti-tumour activity by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance and determining the effect of the candidate substance on the cell, an anti-tumour composition produced by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance, determining the effect of the candidate substance on the cell, identifying a candidate inhibitor substance, and making a composition and an isolated and purified nucleic acid that hybridizes, under high stringency conditions, to a DNA segment comprising about 15-3826 bases of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for altering the phenotype of a tumour cell, for treating cancers (e.g. cancer of the brain, lung, liver, kidney, lymph node, pancreas, small intestine, blood cells, colon, stomach, breast, endometrium, prostate,

CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (p31-p36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene
XX
SQ Sequence 30676 BP; 7591 A; 7621 C; 7888 G; 6944 T; 0 U; 632 Other;
Query Match 53.2%; Score 2037; DB 6; Length 30676;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2327; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 1478 CAGTCCAGCGCCCTAAACCCCTGGACCCGGGACACAGCCCAACAGCGCTGATCCTGTCGG 1537
DB 23420 CAGTCCAGCGCCCTAAACCCCTGGACCCGGGACACAGCCCAACAGCGCTGATCCTGTCGG 23479
QY 1538 ACGACTGCACCAATTGTGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAA 1597
DB 23480 ACGACTGCACCAATTGTGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAA 23539
QY 1598 AGCGCTTCGATGTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1657
DB 23540 AGCGCTTCGATGTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 23599
QY 1658 ACTGGAGGTGGTGGTGGCGAGAGAGACCAAGTGGGTGATCGGGTGGCCACACGAAGCG 1717
DB 23600 ACTGGAGGTGGTGGTGGCGAGAGAGACCAAGTGGGTGATCGGGTGGCCACACGAAGCG 23659
QY 1718 CAAGCCCAAGGCGAGCATCCAGATCCAGCCACGCGCGCTTCTACTGATCGTGATGC 1777
DB 23660 CAAGCCCAAGGCGAGCATCCAGATCCAGCCACGCGCGCTTCTACTGATCGTGATGC 23718
QY 1778 ACGATGCAACAGTACAGCGCTTCAGCGAGCCCTGAGCGGCTTAAAGTCCGGGACA 1837
DB 23719 ACGATGCAACAGTACAGCGCTTCAGCGAGCCCTGAGCGGCTTAAAGTCCGGGACA 23778
QY 1838 AGCTTGACAGGTGGGTGCTTCTGACTATGACCAAGGCTTCTCATCTTCTACCAATG 1897
DB 23779 AGCTTGACAGGTGGGTGCTTCTGACTATGACCAAGGCTTCTCATCTTCTACCAATG 23838
QY 1898 CTGATGACATGCTCTGCTCTACACCTTCGCGAGAGTTCCCTGGCAAGCTCTGCTCTT 1957
DB 23839 CTGATGACATGCTCTGCTCTACACCTTCGCGAGAGTTCCCTGGCAAGCTCTGCTCTT 23898
QY 1958 ACTTCAGCCCTGCGCAGAGCCAGCCAAATGCGAAGACGTTGACCGCTCGGATCAACA 2017
DB 23899 ACTTCAGCCCTGCGCAGAGCCAGCCAAATGCGAAGACGTTGACCGCTCGGATCAACA 23958
QY 2018 CCGTCCGCAATAGTCCAGGCAAGAGACCAACACCTCCTGGGACCACTGCCACTGC 2077
DB 23959 CCGTCCGCAATAGTCCAGGCAAGAGACCAACACCTCCTGGGACCACTGCCACTGC 24018
QY 2078 AAGAGCCCTGCGCAGAGTACAGACCTTGACTCCAGCCCACTGGCCCACTGGAGAC 2137
DB 24019 AAGAGCCCTGCGCAGAGTACAGACCTTGACTCCAGCCCACTGGCCCACTGGAGAC 24077
QY 2138 CTCAGGCCAGTTGTTTACCCCTCCAGCTCCAGTCTGTAATAATGGAGTTGCAATCCCTAC 2197
DB 24078 CTCAGGCCAGTTGTTTACCCCTCCAGCTCCAGTCTGTAATAATGGAGTTGCAATCCCTAC 24137
QY 2198 TTCTTAACTCTCTCCAGCATGATGTTCTGACTCTGACTCTGATAGGATACAGCT 2257
DB 24138 TTCTTAACTCTCTCCAGCATGATGTTCTGACTCTGACTCTGATAGGATACAGCT 24197
QY 2258 TTGATCCAGGATGACATGCTTCTCTAGGGCAACCCCTGCGCCAAACCTCATCCCC 2317
DB 24198 TTGATCCAGGATGACATGCTTCTCTAGGGCAACCCCTGCGCCAAACCTCATCCCC 24257
QY 2318 ATCTTCTCAGGGGACGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA 2377
DB 24258 ATCTTCTCAGGGGACGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA 24317

QY 2378 GGAAGTGTGAGAGCATGGCCAGTAGTTGGCAGCCGAAAGACACACAGCACCTCTTATG 2437
DB 24318 GGAAGTGTGAGAGCATGGCCAGTAGTTGGCAGCCGAAAGACACACAGCACCTCTTATG 24377
QY 2438 TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTATGGGCGAATTTACCTTTGACCCC 2497
DB 24378 TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTATGGGCGAATTTACCTTTGACCCC 24437
QY 2498 AGTCCACAGTGTGTCACAGTAGTACCTGCTCCTGAGGTGGTTCCTGAGAGCAACCTCTCT 2557
DB 24438 AGTCCACAGTGTGTCACAGTAGTACCTGCTCCTGAGGTGGTTCCTGAGAGCAACCTCTCT 24497
QY 2558 GCCACCCCAACACCAAGAACTATATGTTCTTCTCCCACTGATCTGCTGGTCAAGT 2617
DB 24498 GCCACCCCAACACCAAGAACTATATGTTCTTCTTCTCCCACTGATCTGCTGGTCAAGT 24557
QY 2618 ATGATGCTGTGGCTGTGGAAAGGACCTGTGTAGTTAGTCCACACATTTATAGTCATGTC 2677
DB 24558 ATGATGCTGTGGCTGTGGAAAGGACCTGTGTAGTTAGTCCACACATTTATAGTCATGTC 24617
QY 2678 CACCACCTTCTGCTGCCACAGGCCGAGGACAGGGTGGGGTATACCCAAAGCTATGTCAG 2737
DB 24618 CACCACCTTCTGCTGCCACAGGCCGAGGACAGGGTGGGGTATACCCAAAGCTATGTCAG 24677
QY 2738 AGCCCATTAGCTTAAAGCAACTGTCAGGACAAAGCCTCCTGGATGATCGAGGTCCCCAGT 2797
DB 24678 AGCCCATTAGCTTAAAGCAACTGTCAGGACAAAGCCTCCTGGATGATCGAGGTCCCCAGT 24737
QY 2798 AGCTCTCAAGAGTCCAGCAACCTCTTTCAGCCAGGCTCTGTGACCTGTAGGTTG 2857
DB 24738 AGCTCTCAAGAGTCCAGCAACCTCTTTCAGCCAGGCTCTGTGACCTGTAGGTTG 24797
QY 2858 CAGGAGCTTCCAGAGCAGTTGTTGTAATTAGCAACCAAGCTCTGTGAGGAGGCTGTG 2917
DB 24798 CAGGAGCTTCCAGAGCAGTTGTTGTAATTAGCAACCAAGCTCTGTGAGGAGGCTGTG 24857
QY 2918 CTAGACCCCTGTGTCAGACTTGGCATCTATCTCAGTTAGGATCTCTGCTGCAAGAACAGA 2977
DB 24858 CTAGACCCCTGTGTCAGACTTGGCATCTATCTCAGTTAGGATCTCTGCTGCAAGAACAGA 24917
QY 2978 GCCACTGTAGCTGTTTAAATAGACAGGATTTACTACTGGCCCTGTGTGCTGTGCAA 3037
DB 24918 GCCACTGTAGCTGTTTAAATAGACAGGATTTACTACTGGCCCTGTGTGCTGTGCAA 24977
QY 3038 AATTTGTTGAAGAGCTGGAAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGCCGAC 3097
DB 24978 AATTTGTTGAAGAGCTGGAAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGCCGAC 25037
QY 3098 ATTTCATGCTGTGTTGTGACCAAGAAAGCTGCCCATCTGCAAGGAAGCACTATGCA 3157
DB 25038 ATTTCATGCTGTGTTGTGACCAAGAAAGCTGCCCATCTGCAAGGAAGCACTATGCA 25097
QY 3158 GAAAGCTGTGACTGCAAGACTAGGCTCCCTCTGCAACGGTCCGTGCGCAACCAATAGATG 3217
DB 25098 GAAAGCTGTGACTGCAAGACTAGGCTCCCTCTGCAACGGTCCGTGCGCAACCAATAGATG 25157
QY 3218 TCCTAGGCTTCCCTCTCCCACTTCACTCAGTTTCCCAAAATCTAAATTTTACAGAGA 3277
DB 25158 TCCTAGGCTTCCCTCTCCCACTTCACTCAGTTTCCCAAAATCTAAATTTTACAGAGA 25217
QY 3278 TTCTGTTTGGGGAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGAAAT 3337
DB 25218 TTCTGTTTGGGGAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGAAAT 25277
QY 3338 GTCAATTTCCCTAGAGAGTATAGGTTGGGTGGGACCAAGCCCACTGCTGCTTTTCTGCC 3397
DB 25278 GTCAATTTCCCTAGAGAGTATAGGTTGGGTGGGACCAAGCCCACTGCTGCTTTTCTGCC 25337
QY 3398 ACAGCATCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTGTGCTGTC 3457
DB 25338 ACAGCATCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTGTGCTGTC 25397

CC neurodegenerative diseases, or ischaemic disorders.
XX Sequence 2246 BP; 418 A; 805 C; 623 G; 400 T; 0 U; 0 Other;
SQ Query Match 44.3%; Score 1695; DB 9; Length 2246;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGGCTGACCGAAGCGGTGGCTGAAGCTCGCGGGGTGAAGGGTTCGCGTGGG 60
Db 7 AGCTGGCTGACCGAAGCGGTGGCTGAAGCTCGCGGGGTGAAGGGTTCGCGTGGG 66
QY 61 CCAGGGTTTGGGCGCGGATCCGCGAGCTGAGGGGGCGGCACTCTCTCTCTCTG 120
Db 67 CCAGGGTTTGGGCGCGGATCCGCGAGCTGAGGGGGCGGCACTCTCTCTCTG 126
QY 121 GGTACAGCAATGATAGGCTCGGCTGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 180
Db 127 GGTACAGCAATGATAGGCTCGGCTGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 186
QY 181 GCTTCTCGGCTCCCGCCAGCCGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 240
Db 187 GCTTCTCGGCTCCCGCCAGCCGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 246
QY 241 CCCGCTCGGGATCCCGCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCGCCCTAGAA 300
Db 247 CCCGCTCGGGATCCCGCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCGCCCTAGAA 306
QY 301 CCTCCGCTAGGATCTCCGCTCCCTCAGCCGCTCAGAGCTCCCTCCAGCGCCATCGCC 360
Db 307 CCTCCGCTAGGATCTCCGCTCCCTCAGCCGCTCAGAGCTCCCTCCAGCGCCATCGCC 366
QY 361 TTGAGCTGCCCACTACCTTAGAGTCCCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 420
Db 367 TTGAGCTGCCCACTACCTTAGAGTCCCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 426
QY 421 GGGCACCCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 480
Db 427 GGGCACCCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 486
QY 481 TCTTACCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 540
Db 487 TCTTACCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 546
QY 541 GCGCGCGCTCTCTCAGCGCGCCCTCTCGGCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 600
Db 547 GCGCGCGCTCTCTCAGCGCGCCCTCTCGGCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 606
QY 601 GCGATGGCTGAGCTCAAGGAGAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 607 GCGATGGCTGAGCTCAAGGAGAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 666
QY 661 GACCGGTGAGCTGGGCTGGGAGCACTCTCTCGCGCGCTGCTCTCTCTCTCTCTCTCTCT 720
Db 667 GACCGGTGAGCTGGGCTGGGAGCACTCTCTCGCGCGCTGCTCTCTCTCTCTCTCTCTCT 726
QY 721 GTGCGGAGGAGCGCGGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 727 GTGCGGAGGAGCGCGGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 786
QY 781 CCGCGGTGCGCGCGCGCTCAAGCTGCGCAACATCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 787 CCGCGGTGCGCGCGCGCTCAAGCTGCGCAACATCTCTCTCTCTCTCTCTCTCTCTCTCT 846
QY 841 CTGAGCGCACTCTCAAGCGCGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 847 CTGAGCGCACTCTCAAGCGCGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 901 AAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 907 AAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 966
QY 961 CACGAGCAGCATCAGGTTCACCGGATCGACGAGCCCTTCGACGAGTCTCAGAGGAGCTG 1020

CC neurodegenerative diseases, or ischaemic disorders.
XX Sequence 2246 BP; 418 A; 805 C; 623 G; 400 T; 0 U; 0 Other;
SQ Query Match 44.3%; Score 1695; DB 9; Length 2246;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGGCTGACCGAAGCGGTGGCTGAAGCTCGCGGGGTGAAGGGTTCGCGTGGG 60
Db 7 AGCTGGCTGACCGAAGCGGTGGCTGAAGCTCGCGGGGTGAAGGGTTCGCGTGGG 66
QY 61 CCAGGGTTTGGGCGCGGATCCGCGAGCTGAGGGGGCGGCACTCTCTCTCTCTG 120
Db 67 CCAGGGTTTGGGCGCGGATCCGCGAGCTGAGGGGGCGGCACTCTCTCTCTCTG 126
QY 121 GGTACAGCAATGATAGGCTCGGCTGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 180
Db 127 GGTACAGCAATGATAGGCTCGGCTGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 186
QY 181 GCTTCTCGGCTCCCGCCAGCCGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 240
Db 187 GCTTCTCGGCTCCCGCCAGCCGCGGATCCGCGAGCTGAGGGGGTCCCATCCCA 246
QY 241 CCCGCTCGGGATCCCGCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCGCCCTAGAA 300
Db 247 CCCGCTCGGGATCCCGCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCGCCCTAGAA 306
QY 301 CCTCCGCTAGGATCTCCGCTCCCTCAGCCGCTCAGAGCTCCCTCCAGCGCCATCGCC 360
Db 307 CCTCCGCTAGGATCTCCGCTCCCTCAGCCGCTCAGAGCTCCCTCCAGCGCCATCGCC 366
QY 361 TTGAGCTGCCCACTACCTTAGAGTCCCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 420
Db 367 TTGAGCTGCCCACTACCTTAGAGTCCCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 426
QY 421 GGGCACCCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 480
Db 427 GGGCACCCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 486
QY 481 TCTTACCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 540
Db 487 TCTTACCTTCTCTCGGTTACCTCTTCGGAAGCAGACCCCTCTCTCTCTCGGTAGC 546
QY 541 GCGCGCGCTCTCTCAGCGCGCCCTCTCGGCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 600
Db 547 GCGCGCGCTCTCTCAGCGCGCCCTCTCGGCTCCCGGGCTGGGCTCCAGGAGTCTCAGCC 606
QY 601 GCGATGGCTGAGCTCAAGGAGAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 607 GCGATGGCTGAGCTCAAGGAGAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 666
QY 661 GACCGGTGAGCTGGGCTGGGAGCACTCTCTCGCGCGCTGCTCTCTCTCTCTCTCTCTCT 720
Db 667 GACCGGTGAGCTGGGCTGGGAGCACTCTCTCGCGCGCTGCTCTCTCTCTCTCTCTCTCT 726
QY 721 GTGCGGAGGAGCGCGGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 727 GTGCGGAGGAGCGCGGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 786
QY 781 CCGCGGTGCGCGCGCGCTCAAGCTGCGCAACATCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 787 CCGCGGTGCGCGCGCGCTCAAGCTGCGCAACATCTCTCTCTCTCTCTCTCTCTCTCTCT 846
QY 841 CTGAGCGCACTCTCAAGCGCGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 847 CTGAGCGCACTCTCAAGCGCGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 901 AAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 907 AAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 966
QY 961 CACGAGCAGCATCAGGTTCACCGGATCGACGAGCCCTTCGACGAGTCTCAGAGGAGCTG 1020

Db 913 GACGAGCTGCACTGACGAGCAGCATCAGGTACCGGATCGACGAGCCTTCGAGGAG 972
QY 1006 CTGACGAGGAGCTGAGAGGACCAACTTCAGGCCCTTCAAGACAGCGAGCGGGAACACACC 1065
Db 973 CTGACGAGGAGCTGAGAGGACCAACTTCAGGCCCTTCAAGACAGCGAGCGGGAACACACC 1032
QY 1066 GAAGCGCTGAGCTGCTCAAGAGCAAACTGGGAGAGCAAGTCTTCCACCAAGAGCGCTG 1125
Db 1033 GAAGCGCTGAGCTGCTCAAGAGCAAACTGGGAGAGCAAGTCTTCCACCAAGAGCGCTG 1092
QY 1126 CGACGCACTATCGGCGAGGCTTCGAGCGGCTGACCGGCTGCTGCTGAAACGCAAG 1185
Db 1093 CGACCACTATCGGCGAGGCTTCGAGCGGCTGACCGGCTGCTGCTGAAACGCAAG 1152
QY 1186 GCATGCTAGAGGAGCTGAGGCGGACACGCGCCGACGCTGACCGCATCGAGCAAAA 1245
Db 1153 GCATGCTAGAGGAGCTGAGGCGGACACGCGCCGACGCTGACCGCATCGAGCAAAA 1212
QY 1246 GTCCAGCGCTACAGCGAGCTGCGCAAGTCCAGAGGAGCGGAGCTTCCAGGAG 1305
Db 1213 GTCCAGCGCTACAGCGAGCTGCGCAAGTCCAGAGGAGCGGAGCTTCCAGGAG 1272
QY 1306 CGGCTGGCTGAAACGCGGACACACTTCTGGCTGGGCTGCTCACTGTCCGAGCGG 1365
Db 1273 CGGCTGGCTGAAACGCGGACACACTTCTGGCTGGGCTGCTCACTGTCCGAGCGG 1332
QY 1366 CTCAGGGGAAATTCATGAGACCAACCTCATATGAAGACTTCCGACCTCCAGTAC 1425
Db 1333 CTCAGGGGAAATTCATGAGACCAACCTCATATGAAGACTTCCGACCTCCAGTAC 1392
QY 1426 ACAGGCCCTGCGAGTACACATCTGGAAGTCCCTGTTCCAGGACATCCACCTGCGCA 1485
Db 1393 ACAGGCCCTGCGAGTACACATCTGGAAGTCCCTGTTCCAGGACATCCACCTGCGCA 1452
QY 1486 GCGGCCCTTAAACCTGAGCCGCGGACAGCCACAGCGCTGATCTGTGCGAGCACTGC 1545
Db 1453 GCGGCCCTTAAACCTGAGCCGCGGACAGCCACAGCGCTGATCTGTGCGAGCACTGC 1512
QY 1546 ACCATGTGGCTTAGGCAACTTGACCCACAGCACTGCGAGACTGGCCAAAGGCTTC 1605
Db 1513 ACCATGTGGCTTAGGCAACTTGACCCACAGCACTGCGAGACTGGCCAAAGGCTTC 1572
QY 1606 GATGTGGAGGTGCGGTGCTGGTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGGAG 1665
Db 1573 GATGTGGAGGTGCGGTGCTGGTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGGAG 1632
QY 1666 GTGTTGTTGGCGAGAGACCAAGTGGGTGATCGGCTGGCAACAGAGCGCAAGCCCGC 1725
Db 1633 GTGTTGTTGGCGAGAGACCAAGTGGGTGATCGGCTGGCAACAGAGCGCAAGCCCGC 1692
QY 1726 AAGGGCAGCATCCAGATCCAG 1746
Db 1693 AAGGGCAGCATCCAGATCCAG 1713

RESULT 10
ID ADC37264
XX ADC37264 standard; DNA; 2207 BP.
AC ADC37264;
XX
XX
XX 18-DEC-2003 (first entry)
XX Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 97.
XX
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
OS Homo sapiens.
XX

PN WO2003048202-A2.
XX 12-JUN-2003.
XX 03-DEC-2002; 2002WO-JP012644.
XX 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX (ASAH) ASAH KASEI KK.
XX Matsuda A, Muramatsu S;
XX WPI; 2003-505282/47.
XX P-PSDB; ADC37265.
XX New purified protein that activates nuclear factor kappa B (NF-kappaB),
XX useful for treating inflammation, autoimmune diseases, cancers,
XX infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
XX ischemic disorders.
XX Claim 4; SEQ ID NO 97; 938pp; English.
XX The present invention relates to novel proteins and their coding
XX sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
XX kappaB). The proteins and their coding sequences are useful for treating
XX a disease associated with NF-kappaB activation, such as inflammation,
XX autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
XX neurodegenerative diseases, or ischaemic disorders.
XX Sequence 2207 BP; 414 A; 784 C; 618 G; 391 T; 0 U; 0 Other;
SQ
Query Match 32.1%; Score 1230; DB 9; Length 2207;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 466 CCCTTCTCCGCTAGCTCTTACCCCTGCTGTGCGGCTGCTGTCGCGCCCGCCCTC 525
Db 433 CCCTTCTCCGCTAGCTCTTACCCCTGCTGTGCGGCTGCTGTCGCGCCCGCCCTC 492
QY 526 GTGCTGCTTCCAGAGCGCGGCTCTCTCAGCGCGCCCGCCCTGCGCCCGCCCTC 585
Db 493 GTGCTGCTTCCAGAGCGCGGCTCTCTCAGCGCGCCCGCCCTGCGCCCGCCCTC 552
QY 586 TCTGCTGCTTCCAGAGCGCGGCTCTCTCAGCGCGCCCGCCCTGCGCCCGCCCTC 645
Db 553 TCTGCTGCTTCCAGAGCGCGGCTCTCTCAGCGCGCCCGCCCTGCGCCCGCCCTC 612
QY 646 CTGAGCATCTACAGGACCCGCTGAGCTTGGGCTGCGAGCATCTACTTCTGCGCGCTGC 705
Db 613 CTGAGCATCTACAGGACCCGCTGAGCTTGGGCTGCGAGCATCTACTTCTGCGCGCTGC 672
QY 706 ATCAGCGAGCATCTGGTGGGCTGAGGAGCGCGGCGCGGCTGCGCCCGAGTGC 765
Db 673 ATCAGCGAGCATCTGGTGGGCTGAGGAGCGCGGCGCGGCTGCGCCCGAGTGC 732
QY 766 CGCAGCTTCCGCGAGCGCGCTGCGCGCCCGAGCTCAAGCTGGCCCAACATCTGAGAGCGC 825
Db 733 CGCAGCTTCCGCGAGCGCGCTGCGCGCCCGAGCTCAAGCTGGCCCAACATCTGAGAGCGC 792
QY 826 TACAGCTTCTTCCGCTGAGCGCATCTCAACGCGCGCGCGCGCGCGCGCTGCAG 885
Db 793 TACAGCTTCTTCCGCTGAGCGCATCTCAACGCGCGCGCGCGCGCGCGCTGCAG 852
QY 886 GCGCAGCAGAGCTCAAGCTTCTGCTCAGCAGCGCGCTTCTCTGCTTCTTCTGC 945
Db 853 GCGCAGCAGAGCTCAAGCTTCTGCTCAGCAGCGCGCTTCTCTGCTTCTTCTGC 912
QY 946 GACGAGCTTCTGCTGACGAGCAGCATCAGTCAACCGGATTCAGCAGCGCTTGCAG 1005
Db 913 GACGAGCTTCTGCTGACGAGCAGCATCAGTCAACCGGATTCAGCAGCGCTTGCAG 972

PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 35438; 3071pp + Sequence Listing; English.
PS
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to prevent,
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and
CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 5858 BP; 1481 A; 1575 C; 1462 G; 1340 T; 0 U; 0 Other;
Query Match 24.3%; Score 928; DB 4; Length 5858;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 2148 TTGTTTACCTCCAGCCTCCAGTCTGTAATGAGGTTGCAATCCCTACTTCTCTAACT 2207
DB 674 TTGTTTACCTCCAGCCTCCAGTCTGTAATGAGGTTGCAATCCCTACTTCTCTAACT 733
QY 2208 CTCCTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCTTGTATCCAAAG 2267
DB 734 CTCCTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCTTGTATCCAAAG 793
QY 2268 GATGTGACATGGCTTCTCTCAGGGCAACCCCTGCCAACCCCTGATCCCATCTTCTCAG 2327
DB 794 GATGTGACATGGCTTCTCTCAGGGCAACCCCTGCCAACCCCTGATCCCATCTTCTCAG 853
QY 2328 GGGCAGGGGACTACCTTCCAGTGTCTCCTCCAGCCCGAGCCCTGACCTCAGGAAGTGTCA 2387
DB 854 GGGCAGGGGACTACCTTCCAGTGTCTCCTCCAGCCCGAGCCCTGACCTCAGGAAGTGTCA 913
QY 2388 GAGCATGGCCAGTAGTTGGCAGCCCGAAGACACACAGCACCCCTTATGTCCATGGCC 2447
DB 914 GAGCATGGCCAGTAGTTGGCAGCCCGAAGACACACAGCACCCCTTATGTCCATGGCC 973
QY 2448 TAAGACTTACCCCTGACCAAGCTAGTGTGGGCAATTTACCTTGACCCCGAGTCCACAGT 2507
DB 974 TAAGACTTACCCCTGACCAAGCTAGTGTGGGCAATTTACCTTGACCCCGAGTCCACAGT 1033
QY 2508 GGTACAGGTAGTACCTGGTCTTAGGGTTGCTGAGAGCAACCTCTCTGACCCCGAGTCCAC 2567
DB 1034 GGTACAGGTAGTACCTGGTCTTAGGGTTGCTGAGAGCAACCTCTCTGACCCCGAGTCCAC 1093
QY 2568 CACCAAGAACTATATGTTCTTACTTCTCCACTGATCTGCTGGTCAAGTATGCTGT 2627
DB 1094 CACCAAGAACTATATGTTCTTACTTCTCCACTGATCTGCTGGTCAAGTATGCTGT 1153
QY 2628 GGCCTGTGGAAGGCACCTGTAGTTCAGTCCACATATAGTCAATGATGTCACCAACCTTC 2687
DB 1154 GGCCTGTGGAAGGCACCTGTAGTTCAGTTCAGTCCACATATAGTCAATGATGTCACCAACCTTC 1213
QY 2688 CTGCCACAGCCGAGGACAGGGTATAGGATATACCAAGCTGATGACAGGCCATTAG 2747
DB 1214 CTGCCACAGCCGAGGACAGGGTATAGGATATACCAAGCTGATGACAGGCCATTAG 1273
QY 2748 CCTAAAGCAACTGCAGGACCAAGCTCTCTGGATGATCGAGTCCCGAGTCTCTGAAC 2807
DB 1274 CCTAAAGCAACTGCAGGACCAAGCTCTCTGGATGATCGAGTCCCGAGTCTCTGAAC 1333
QY 2808 AAGAGTCCAGCAACCCCTCTTCAGCCAGGCTCTGTGACCTGTCTGAGGTGAGGAGGCTT 2867

PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
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PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
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PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
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PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483426/52.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,

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Db 1334 AAGAGTCCAGGCAACCCCTCTTCAGCAGGCGCTCTGTACCTGTCTAGGTCGAGGAGGCTT 1393
Qy 2868 CCAGAAAGCAGTTGTTGTAATAGGACCCCAAGCACT- GGGAGGGGCTGTGTGGCTAGACCCC 2926
Db 1394 CCAGAACAGTGTTGTTGTAATAGGACCCCAAGCACTGGGGGAGGGGCTGTGGCTAAACCCC 1453
Qy 2927 TTGTCAGACTTTGGCATCTATCTCAGTTAGGATCCCTGCTGCAGAAAACAAGACCACTGTT 2986
Db 1454 TTGTCAGACTTTGGCATCTATCTCAGTTAGGATCCCTGCTGCAGAAAACAAGACCACTGTT 1513
Qy 2987 AGCTGGTTTAAATTAGACAGAGATTATCTACCTGGCCCTCGTGGCTTGCAAAATTTGTTGG 3046
Db 1514 AGCTGGTTTAAATTAGACAGAGATTATCTACCTGGCCCTCGTGGCTTGCAAAATTTGTTGG 1573
Qy 3047 AAGAGCTGGAGAACAGACTCTGCTGAATTTCCAGGAATCTCCAGCGCCAGATTCATCAT 3106
Db 1574 AAGAGCTGGAGAACAGACTCTGCTGAATTTCCAGGAATCTCCAGCGCCAGATTCATCAT 1633
Qy 3107 GTCTGTTGTGACAGAAAGCTGCCCCATCTGCAGGAAGCACTATGCCAGAAAGCTGC 3166
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Qy 3167 TGACTGAGAACTAGGCTCCCTCTGCGACAGCGTCCGTGCGACCAATAGATGCTCTGAGGC 3226
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Qy 3227 CTGCCCCCTCTCCCACTTCACTCAGTCTCCCAATCTAAATTTTACAGAGATTCCTGTTG 3286
Db 1754 CTGCCCCCTCTCCCACTTCACTCAGTCTCCCAATCTAAATTTTACAGAGATTCCTGTTG 1813
Qy 3287 GGGGAACCTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAATGTCATTTC 3346
Db 1814 GGGGAACCTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAATGTCATTTC 1873
Qy 3347 CTAGAGGAAGTTAGGTGGTGAGCAAGCCACCTCGCTTTTCTGCCAGACATCC 3406
Db 1874 CTAGAGGAAGTTAGGTGGTGAGCAAGCCACCTCGCTTTTCTGCCAGACATCC 1933
Qy 3407 AATCGTGAACAACCTCGGAGAGGTGAGTCCATCATCTAGGGTGTCTGCCCCCTGGCT 3466
Db 1934 AATCGTGAACAACCTCGGAGAGGTGAGTCCATCATCTAGGGTGTCTGCCCCCTGGCT 1993
Qy 3467 CTATCCCTGCCAGAGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGGCTAAATGTCT 3526
Db 1994 CTATCCCTGCCAGAGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGGCTAAATGTCT 2053
Qy 3527 CCCCAGCCTTGACTTTCTTCTAGTCTGGGCTAGATCTGCACTTGGGCTCTGA 3586
Db 2054 CCCCAGCCTTGACTTTCTTCTAGTCTGGGCTAGATCTGCACTTGGGCTCTGA 2113
Qy 3587 CACAACACACCATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGTTCTTAAATGGCT 3646
Db 2114 CACAACACACCATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGTTCTTAAATGGCT 2173
Qy 3647 GCCCCGCCACCGGGGCTCCCTTGGGCAAAAGGAATTTGTACGCCCTACCCCAACCCCTC 3706
Db 2174 GCCCCGCCACCGGGGCTCCCTTGGGCAAAAGGAATTTGTACGCCCTACCCCAACCCCTC 2233
Qy 3707 AACTACCAAGTGGGCCACCCAGAGTATTTTATTAAGTTGTCCTATTTATG 3766
Db 2234 AACTACCAAGTGGGCCACCCAGAGTATTTTATTAAGTTGTCCTATTTATG 2293
Qy 3767 AGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA 3807
Db 2294 AGTTATGATCAATTTCTATTAAATTAAGTTACAGATGCA 2334
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RESULT 12

ABK12808

ID ABK12808 standard; DNA; 30625 BP.

XX

AC ABK12808;

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XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor CAR-1, BAC clone 392H05 3' sequence.
XX
KW Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteria artificial chromosome; chromosome lp31-lp36.
XX
OS Homo sapiens.
XX
FN WO200212285-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
PR 10-AUG-2000; 2000US-0225033P.
XX
PR 23-AUG-2000; 2000US-0227560P.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Killary A, Chandler D, Lott S;
XX
DR WPI; 2002-269088/31.
XX
PT New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
PS Disclosure; Page 149-157; 185pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumor suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (lp31-lp36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene
```

XX	SQ	Sequence 30625 BP; 8084 A; 7712 C; 7487 G; 7314 T; 0 U; 28 Other;	
		Query Match 24.3%; Score 928; DB 6; Length 30625;	
		Best Local Similarity 99.2%; Pred. No. 0;	
		Matches 1648; Conservative 0; Mismatches 12; Indels 1; Gaps 1;	
QY	2148	TTGTTTACCCCTCCAGCCTCCAGTCTGTAATAAGAGGTTGATTCCTTCTAACT 2207	
DB	22623	TTGTTTACCCCTCCAGCCTCCAGTCTGTAATAAGAGGTTGATTCCTTCTAACT 22682	
QY	2208	CTCTTCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCTTTGATCCAAG 2267	
DB	22683	CTCTTCAGCATCGATGTTCTGTACCTCTGACCTTGATAGGAAACAGCTTTGATCCAAG 22742	
QY	2268	GATGTGATGCTGCTTCCTCAGGGCAACCCCTCCCAACCCCTCATCCCATCTTCTCAG 2327	
DB	22743	GATGTGATGCTGCTTCCTCAGGGCAACCCCTCCCAACCCCTCATCCCATCTTCTCAG 22802	
QY	2328	GGGAGGGGACTACTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTC 2387	
DB	22803	GGGAGGGGACTACTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTC 22862	
QY	2388	GAGCATGGCAGTATGGGAGCCGGAAGACACACAGCACCCCTTATGTCCTCATGGCC 2447	
DB	22863	GAGCATGGCAGTATGGGAGCCGGAAGACACACAGCACCCCTTATGTCCTCATGGCC 22922	
QY	2448	TAAGACTTACCCCTGACCAAGCTAGTGATGGGCCATTTACCCCTTGACCCCAAGTCCACAGT 2507	
DB	22923	TAAGACTTACCCCTGACCAAGCTAGTGATGGGCCATTTACCCCTTGACCCCAAGTCCACAGT 22982	
QY	2508	GGTCACAGGTAGTACTGGTCTCCTAGGTTGCTGAGAGCAACCTCTCTGCGACCCCA 2567	
DB	22983	GGTCACAGGTAGTACTGGTCTCCTAGGTTGCTGAGAGCAACCTCTCTGCGACCCCA 23042	
QY	2568	CACCAAGACTATATGGTCTTCTACTTCTCCCACTCATCTGTGTGTCAGTGATGCTGT 2627	
DB	23043	CACCAAGAAATATATGGTCTTCTACTTCTCCCACTCATCTGTGTGTCAGTGATGCTGT 23102	
QY	2628	GGCTGTGGAAGGCACTGGTATGTTGAGTCCACACATTATAGTATGTCGCCACCCCTTC 2687	
DB	23103	GGCTGTGGAAGGCACTGGTATGTTGAAATCCACACATTATAGTATGTCGCCACCCCTTC 23162	
QY	2688	CTGCCACAGGCGGAGGACAGGGTGAGGTTATCCAAAGCTGATGACAGCCCATTTAG 2747	
DB	23163	CTGCCACAGGCGGAGGACAGGGTGAGGTTATCCAAAGCTGATGACAGCCCATTTAG 23222	
QY	2748	CCTAAAGCAACTGACAGGACAGCCCTCCTGGATGATCAGGTCCCCAGTAGCTCTGAAC 2807	
DB	23223	CCTAAAGCAACTGACAGGACAGCCCTCCTGGATGATCAGGTCCCCAGTAGCTCTGAAC 23282	
QY	2808	AAGAGTCCAGCAACCCCTCTCAGCCAGGCTCTGTGACCTGTAGGCTGACGAGGCTT 2867	
DB	23283	AAGAGTCCAGCAACCCCTCTCAGCCAGGCTCTGTGACCTGTAGGCTGACGAGGCTT 23342	
QY	2868	CCAGAAGGAGTGTGTTGTAATTAGGACCCAGCACT-GGGAGGGGCTGTGGCTAGACCCC 2926	
DB	23343	CCAGAAGGAGTGTGTTGTAATTAGGACCCAGCACTGGGAGGGGCTGTGGCTTAACCCC 23402	
QY	2927	TTGTGACAGTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAAAAACAAGAGCCATTGT 2986	
DB	23403	TTGTGACAGTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAAAAACAAGAGCCATTGT 23462	
QY	2987	AGCTGGTTTTAATPAGCAAGGATTTACTACTGGCCCTGTGGCTGTGCAAAATGTTGG 3046	
DB	23463	AGCTGGTTTTAATPAGCAAGGATTTACTACTGGCCCTGTGGCTGTGCAAAATGTTGG 23522	
QY	3047	AAGAGCTGGAGAGCAGACTCTGTAATTTCCAGGAACCTCCAGCCAGGATTCATCAT 3106	
DB	23523	AAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGCCAGGATTCATCAT 23582	
QY	3107	GTCTGTGTGTGACCAAGAAAGCTGCCCCCATCTGCGAAGCCCATATGCGCAGAAAGCTGC 3166	

DB	23583	GTCTGTGTGTGACCAAGAAAGCTGCCCCCATCTCGAGGAAGCCACTATGCCAGAAAGCTGC 23642	
QY	3167	TGACTGCAGAACTAGGCTCCCTCTGCCAGGTCGTCGCCAGCAATAGATGTCTCTGAGGC 3226	
DB	23643	TGACTGCAGAACTAGGCTCCCTCTGCCAGGTCGTCGCCAGCAATAGATGTCTCTGAGGC 23702	
QY	3227	CTGCCCCCTCTCCACATTTCACTCAGTTTCCAAAATCTAAATTTTACAAGAGATTCTGTTG 3286	
DB	23703	CTGCCCCCTCTCCACATTTCACTCAGTTTCCAAAATCTAAATTTTACAAGAGATTCTGTTG 23762	
QY	3287	GGGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGCTCGGGAATGTCATTTCC 3346	
DB	23763	GGGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGCTCGGGAATGTCATTTCC 23822	
QY	3347	CTAGAAGGAAGTTAGGCTGGGTGGAGCAAGCCCACTCGCTGCTTTTCTGCCACAGCATCC 3406	
DB	23823	CTAGAAGGAAGTTAGGCTGGGTGGAGCAAGCCCACTCGCTGCTTTTCTGCCACAGCATCC 23882	
QY	3407	AATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCTGCCCTTGGCT 3466	
DB	23883	AATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCTGCCCTTGGCT 23942	
QY	3467	CTATCCCTGCCCCAGAGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGCCTTAATGTC 3526	
DB	23943	CTATCCCTGCCCCAGAGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGCCTTAATGTC 24002	
QY	3527	CCCCGGCCTTACATTTTCTTTCTAGTCTGGGGCTAGATTTCTGCACCTTGGGGTCTCTGA 3586	
DB	24003	CCCCGGCCTTACATTTTCTTTCTAGTCTGGGGCTAGATTTCTGCACCTTGGGGTCTCTGA 24062	
QY	3587	CACAACACACCATCCCAAAGTAGCGGGAAGAGCTTAAACACAGGGGGTCTTTAAATGGCT 3646	
DB	24063	CACAACACACCATCCCAAAGTAGCGGGAAGAGCTTAAACACAGGGGGTCTTTAAATGGCT 24122	
QY	3647	GGCCCCGCCACCCGGGCTCTCTTGGGCAAGGAATGTGACGCCCTACCCCAACCCCTTC 3706	
DB	24123	GGCCCCGCCACCCGGGCTCTCTTGGGCAAGGAATGTGACGCCCTACCCCAACCCCTTC 24182	
QY	3707	AACTACCAAGATCTGGGCCACCCCAAGCAGTATTTTATTTAAATGTTGCCCATTTATG 3766	
DB	24183	AACTACCAAGATCTGGGCCACCCCAAGCAGTATTTTATTTAAATGTTGCCCATTTATG 24242	
QY	3767	AGTTATGATCAATTTGTTATTAATTAAGTTAAAGTTACAGATGTCA 3807	
DB	24243	AGTTATGATCAATTTGTTATTAATTAAGTTAAAGTTACAGATGTCA 24283	
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ABK12809			
ID	ABK12809	standard; DNA; 45845 BP.	
XX	AC	ABK12809;	
XX	DT	18-JUN-2002 (first entry)	
XX	DE	Human tumour suppressor CAR-1, BAC clone RP11-150F21 5' sequence.	
XX	KW	Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;	
XX	KW	gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;	
XX	KW	colon cancer; stomach cancer; breast cancer; endometrial cancer;	
XX	KW	prostate cancer; testicular cancer; ovarian cancer; skin cancer;	
XX	KW	head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;	
XX	XX	bacteria artificial chromosome; chromosome 1p31-1p36.	
XX	OS	Homo sapiens.	
XX	PN	WO200212285-A2.	
XX	PD	14-FEB-2002.	
XX	PF	09-AUG-2001; 2001WO-US025269.	
XX	PF	10-AUG-2000; 2000US-0225033P.	

Db	301	AGCGTGGCGTGCAGCACTACTTCTTGC	CGCGCGCTGCATCA	CGGAGCACTGGGTGGCGGAG	361					
Qy	730	GAGCGCAGGCGCGCCCGCACTGCCCGAGTGC	CGCGCGCACTGTTCCGCGAGCCCGCGCTG	789						
Db	361	GAGCGCAGGCGCGCCCGCACTGCCCGAGTGC	CGCGCGCACTGTTCCGCGAGCCCGCGCTG	420						
Qy	790	GCGCCAGCCCTCAAGCTGGCCAAACATCGTGG	AGCGGTACAGCTCTTCCCGCTGGACGCC	849						
Db	421	GCGCCAGCCCTCAAGCTGGCCAAACATCGTGG	AGCGGTACAGCTCTTCCCGCTGGACGCC	480						
Qy	850	ATCCTCAACGGCGCGCGCGCGCGCGCGCGCG	CGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	902						
Db	481	ATCCTCAACGGCGCGCGCGCGCGCGCGCGCG	CGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	533						
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AA116850/c										
ID	AA116850 standard; DNA; 573 BP.									
XX	AA116850;									
XX	12-OCT-2001 (first entry)									
DE	Probe #6783 for gene expression analysis in human cervical cell sample.									
XX	Probe; human; microarray; gene expression; cervical epithelial cell;									
KW	cervical cancer; ss.									
XX	Homo sapiens.									
OS	Homo sapiens.									
FN	WO200157278-A2.									
XX	09-AUG-2001.									
PD	09-AUG-2001.									
XX	30-JAN-2001; 2001WO-US000670.									
PF	30-JAN-2001; 2001WO-US000670.									
XX	04-FEB-2000; 2000US-0180312P.									
PR	26-MAY-2000; 2000US-0207456P.									
PR	30-JUN-2000; 2000US-00608408.									
PR	03-AUG-2000; 2000US-00632366.									
PR	21-SEP-2000; 2000US-0234687P.									
PR	27-SEP-2000; 2000US-0236359P.									
PR	04-OCT-2000; 2000GB-00024263.									
XX	(MOLE-) MOLECULAR DYNAMICS INC.									
PA	(MOLE-) MOLECULAR DYNAMICS INC.									
XX	Penn SG, Hanzel DK, Chen W, Rank DR;									
PI	Penn SG, Hanzel DK, Chen W, Rank DR;									
XX	WPI; 2001-488901/53.									
DR	WPI; 2001-488901/53.									
XX	Human genome-derived single exon nucleic acid probes useful for analyzing									
PT	gene expression in human cervical epithelial cells.									
XX	Claim 25; SEQ ID NO 6783; 487bp; English.									
PS	Claim 25; SEQ ID NO 6783; 487bp; English.									
XX	The present invention relates to human single exon nucleic acid probes									
CC	(SENP). The present sequence is one such probe. The SENPs are derived									
CC	from human HeLa cells. The SENPs can be used to produce a single exon									
CC	microarray, which can be used for measuring human gene expression in a									
CC	sample derived from human cervical epithelial cells. By measuring gene									
CC	expression, the probes are therefore useful in grading and/or staging of									
CC	diseases of the cervix, notably cervical cancer. Note: The sequence data									
CC	for this patent did not form part of the printed specification, but was									
CC	obtained in electronic format directly from WIPO at									
CC	ftp.wipo.int/pub/published_pct_sequences									
XX	Sequence 573 BP; 109 A; 164 C; 179 G; 121 T; 0 U; 0 Other;									
SQ	Sequence 573 BP; 109 A; 164 C; 179 G; 121 T; 0 U; 0 Other;									
Query Match										
Best Local Similarity 100.0%; Score 493; DB 4; Length 573;										
Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;										
Qy	1602	CTTCGATGTGAGGTGTGGTGGTCTTCAAGCC								

Db	573	CTTCGATGTGGAGGTGTTCGGTGTGGGTCTGAAGCCTTCAGTAGTGGCGTCACACTG	514
QY	1662	GGAGGTGGTGGCGGAGAAACCCAGTGGGTGATCGGGCTGGCACAGAACCCCAAG	1721
Db	513	GGAGGTGGTGGCGGAGAAACCCAGTGGGTGATCGGGCTGGCACAGAACCCCAAG	454
QY	1722	CCGCAAGGGCAGCATCCAGATCCAGGCCAGCCCGCGGTCTTACTGTCATCGTGTGACACGA	1781
Db	453	CCGCAAGGGCAGCATCCAGATCCAGGCCAGCCCGCGGTCTTACTGTCATCGTGTGACACGA	394
QY	1782	TGSCAACCAAGTACAGCGCCTGCACGGAGCCCTGGACCGCGCTTAAAGTCCGGGACAAAGCT	1841
Db	393	TGSCAACCAAGTACAGCGCCTGCACGGAGCCCTGGACCGCGCTTAAAGTCCGGGACAAAGCT	334
QY	1842	TGACAAAGTGGGTGCTTCTCTGGACTATGACCAAGGCTTGCTCATCTTCTACAAATGCTGA	1901
Db	333	TGACAAAGTGGGTGCTTCTCTGGACTATGACCAAGGCTTGCTCATCTTCTACAAATGCTGA	274
QY	1902	TGCATGTCTTGCTCTTACACCTTCGCGAGAAAGTTCCCTGGCAAGCTTGCTCTTACTTT	1961
Db	273	TGCATGTCTTGCTCTTACACCTTCGCGAGAAAGTTCCCTGGCAAGCTTGCTCTTACTTT	214
QY	1962	CAGCCTGGCCAGNGCCACGCCAATGCRAGAAGCTTCAGCCGCTGGGATCAACACCGT	2021
Db	213	CAGCCTGGCCAGNGCCACGCCAATGCRAGAAGCTTCAGCCGCTGGGATCAACACCGT	154
QY	2022	CCGCATCTAGTTCAGGCAGAGGAGACCAACCTCTCTGGGACACTGCCACCTGCAAGA	2081
Db	153	CCGCATCTAGTTCAGGCAGAGGAGACCAACCTCTCTGGGACACTGCCACCTGCAAGA	94
QY	2082	GCCTGCCACGA	2094
Db	93	GCCTGCCACGA	81

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: /cgn2.6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2.6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2.6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2.6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	0.7	469	1	US-08-468-347-23
2	25	0.7	469	1	US-08-226-264-25
3	25	0.7	469	1	US-08-467-389-23
4	25	0.7	469	2	US-08-779-379-23
5	25	0.7	469	2	US-08-469-219-23
6	25	0.7	469	3	US-08-228-152-23
7	25	0.7	729	1	US-08-447-010-1
8	25	0.7	868	3	US-08-889-502-20
9	25	0.7	9844	4	US-09-791-211-10
10	24	0.6	40	3	US-09-306-290-26
11	24	0.6	555	4	US-09-449-285A-15
12	24	0.6	1196	3	US-07-959-509-4
13	24	0.6	1332	3	US-09-333-423-1
14	24	0.6	1392	4	US-08-957-351-1
15	24	0.6	1478	4	US-09-216-393B-7
16	24	0.6	1496	4	US-09-712-529-1
17	24	0.6	1628	2	US-08-883-515-3
18	24	0.6	1705	4	US-09-205-258-216
19	24	0.6	2017	3	US-09-436-983-1
20	24	0.6	2193	4	US-09-427-261-2
21	24	0.6	2193	4	US-09-427-261-3
22	24	0.6	3001	4	US-09-539-333D-222
23	24	0.6	3848	3	US-09-112-096-28
24	24	0.6	3952	2	US-08-381-691-16
25	24	0.6	5668	3	US-09-112-096-14
26	24	0.6	5668	4	US-09-636-215-777
27	24	0.6	5668	4	US-09-685-166A-777

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Sequence 3, Appli
Sequence 44, Appli
Sequence 63, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 15, Appli
Sequence 10956, A
Sequence 9086, Ap
Sequence 28, Appl
Sequence 15342, A
Sequence 13, Appl
Sequence 6, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 17, Appli

24 0.6 21234 4 US-09-810-671-3
24 0.6 21234 4 US-10-109-854-3
24 0.6 32042 4 US-09-245-281-44
24 0.6 32042 4 US-09-340-620A-63
24 0.6 50000 4 US-08-146-053-3
24 0.6 786431 4 US-09-751-389-3
23 0.6 40 3 US-09-306-290-15
23 0.6 67 4 US-09-621-976-10956
23 0.6 97 4 US-09-621-976-9086
23 0.6 307 4 US-09-091-725-28
23 0.6 350 4 US-09-621-976-15342
23 0.6 433 1 US-07-987-272A-13
23 0.6 567 1 US-08-661-168-6
23 0.6 627 3 US-09-385-982-4
23 0.6 989 2 US-08-874-460-1
23 0.6 989 4 US-09-272-162-1
23 0.6 1005 4 US-09-647-224A-5
23 0.6 1087 4 US-09-396-149-17

ALIGNMENTS

RESULT 1
US-08-468-347-23
; Sequence 23, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-468-347-23

Query Match 0.7%; Score 25; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.37;

us-09-927-091-3.oli15.rni

Mon Aug 2 10:03:35 2004

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
 Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 2

US-08-226-264-25
 ; Sequence 25, Application US/08226264
 ; Patent No. 5801017
 ; GENERAL INFORMATION:
 ; APPLICANT: Werber, Moshe M.
 ; APPLICANT: Zeelon, Elisha P.
 ; APPLICANT: Levanon, Avigdor
 ; APPLICANT: Guy, Rachel
 ; APPLICANT: Goldlust, Arie
 ; APPLICANT: Rigbi, Meir
 ; APPLICANT: Panet, Amos
 ; APPLICANT: Fischer, Meir
 ; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
 ; TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/226.264
 ; FILING DATE: 08-APR-94
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 469 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-226-264-25

Query Match 0.7%; Score 25; DB 1; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
 Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 3

US-08-467-389-23
 ; Sequence 23, Application US/08467389
 ; Patent No. 5824641
 ; GENERAL INFORMATION:
 ; APPLICANT: Zeelon, Elisha P.

APPLICANT: Werber, Moshe M.
 APPLICANT: Levanon, Avigdor
 TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
 TITLE OF INVENTION: INHIBITORY ACTIVITY
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 ZIP: 10112

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,389
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/225,442
 FILING DATE: 08-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-977-9550
 TELEFAX: 212-664-0525
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-467-389-23

Query Match 0.7%; Score 25; DB 1; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
 Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 4

US-08-779-379-23
 ; Sequence 23, Application US/08779379
 ; Patent No. 5858970
 ; GENERAL INFORMATION:
 ; APPLICANT: Zeelon, Elisha P.
 ; APPLICANT: Werber, Moshe M.
 ; APPLICANT: Levanon, Avigdor
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
 ; TITLE OF INVENTION: INHIBITORY ACTIVITY
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,379
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-779-379-23

Query Match 0.7%; Score 25; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. NO. 0.37;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
DB 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 5
US-08-469-219-23
Sequence 23, Application US/08469219
Patent No. 5863534
GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
TITLE OF INVENTION: INHIBITORY ACTIVITY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,219
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 469 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-469-219-23

Query Match 0.7%; Score 25; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. NO. 0.37;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
DB 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 6
US-09-228-152-23
Sequence 23, Application US/09228152
Patent No. 6211341
GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY
FILE REFERENCE: 43020aya
CURRENT APPLICATION NUMBER: US/09/228,152
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 469
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
OTHER INFORMATION: of clone pSP65-Xa1-4.
US-09-228-152-23

Query Match 0.7%; Score 25; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. NO. 0.37;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
DB 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 7
US-08-447-010-1
Sequence 1, Application US/08447010
Patent No. 5770718
GENERAL INFORMATION:
APPLICANT: MOFFATT, BARBARA
TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, Suite 701
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/447,010
FILING DATE: 22-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/230,695
FILING DATE: 21-APR-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,132
FILING DATE: 26-MAY-1992
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1811-183 MIS:vg
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(18..569)
US-08-447-010-1

Query Match 0.7%; Score 25; DB 1; Length 729;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3802 ATGTCACAAAAA 3826
Db 705 ATGTCACAAAAA 729

RESULT 8
US-08-889-502-20
Sequence 20, Application US/0889502
Patent No. 6066726
GENERAL INFORMATION:
APPLICANT: Barb, David H
APPLICANT: Russek, Shelley J
TITLE OF INVENTION: GENE THERAPY VECTOR WITH TISSUE
SPECIFICITY
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,502
FILING DATE: 08-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: 0146-2008
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 868 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-889-502-20

Query Match 0.7%; Score 25; DB 3; Length 868;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3802 ATGTCACAAAAA 3826
Db 440 ATGTCACAAAAA 464

RESULT 9
US-09-791-211-10/c
Sequence 10, Application US/09791211
Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 98844
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 24962
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 64383
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65468
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65469
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 87130
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 89049
OTHER INFORMATION: unknown
OTHER INFORMATION:
US-09-791-211-10

Query Match 0.7%; Score 25; DB 4; Length 98844;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3802 ATGTCACAAAAA 3826
Db 95450 ATGTCACAAAAA 95426

RESULT 10
US-09-306-290-26/c


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; Sequence 26, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; APPLICANT: Mukhopadhyay, Sunil
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
; TITLE OF INVENTION: (SPADT) USING MULTIARRAYS
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer p41
; OTHER INFORMATION: FH440
US-09-306-290-26

Query Match          0.6%; Score 24; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 24 TGTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11
US-09-449-285A-15/c
; Sequence 15, Application US/09449285A
; Patent No. 6313280
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie
; TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
; FILE REFERENCE: 2676-4232US
; CURRENT APPLICATION NUMBER: US/09/449,285A
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: PCT/EP98/03193
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 97201645.5
; PRIOR FILING DATE: 1997-06-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (382)..(555)
; OTHER INFORMATION: n can be any nucleotide
US-09-449-285A-15

Query Match          0.6%; Score 24; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 24 TGTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 12
US-07-959-509-4
; Sequence 4, Application US/07959509
; Patent No. 6001560
; GENERAL INFORMATION:
; APPLICANT: Ionial, Herinder
; APPLICANT: Narula, Satwanti
; APPLICANT: Zavodny, Paul
```

```
; TITLE OF INVENTION: Human Gamma Interferon Antagonist/Agonist Screen
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 4.00B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,509
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/616,621
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dulak, No. 6001560man C.
; REGISTRATION NUMBER: 31,608
; REFERENCE/DOCKET NUMBER: JB0166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 822 7375
; TELEFAX: 201 822 7039
; TELEX: 219165
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-959-509-4

Query Match          0.6%; Score 24; DB 3; Length 1196;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 327 TGTCAAAAAAAAAAAAAAAAAAAAAA 350

RESULT 13
US-09-333-423-1
; Sequence 1, Application US/09333423
; Patent No. 6265636
; GENERAL INFORMATION:
; APPLICANT: Randall, Douglas
; APPLICANT: Thelen, Jay
; APPLICANT: Miernyk, Jan
; APPLICANT: Muszynski, Michael
; APPLICANT: Sewalt, Vincent
; TITLE OF INVENTION: Pyruvate Dehydrogenase Kinase
; TITLE OF INVENTION: Polynucleotides, Polypeptides and Uses Thereof
; FILE REFERENCE: 0818
; CURRENT APPLICATION NUMBER: US/09/333,423
; CURRENT FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,998
; EARLIER FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)...(1095)
US-09-333-423-1
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Query Match          0.6%; Score 24; DB 3; Length 1332;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
    |||
Db 1279 TGTCAAAAAAAAAAAAAAAAAAAAAA 1302

RESULT 14
US-08-957-351-1
; Sequence 1, Application US/08957351
; Patent No. 6306586
; GENERAL INFORMATION:
; APPLICANT: Semina, Elena
; APPLICANT: Murray, Jeffrey C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CATARACTS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,351
; FILING DATE: 24-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-024.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-957-351-1

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Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1369 TGTCAAAAAAAAAAAAAAAAAAAAAA 1392

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; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
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; TYPE: DNA
; ORGANISM: Toxoplasma gondii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1161)
; OTHER INFORMATION:
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1427 TGTCAAAAAAAAAAAAAAAAAAAAAA 1450

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Job time : 248 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 05:58:02 ; Search time 1597 Seconds
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Gapop 60.0 , Gapext 60.0

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Word size : 15

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	431	11.3	431	9	US-09-864-761-23962
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ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3826
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-3

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						Gaps	0;
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; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: US/09/927,091
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (5071)..(23433)
; OTHER INFORMATION: n = A or C or G or T/U
US-09-927-091-7

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QY	2078	AAGAGCCCTGCCAGAGAAATAGAGACCTGTGACTCCAGCCACCGTGGCCACTGGAGAC	2137	Db	14208	GAAGCTGTGACTGCAGAACTAGGCTCCCTCTGCAACGGTCCGTCAGCCCAATAGATG	14267
Db	13129	AAGAGCCCTGCCAGAGAAATAGAGACCTGTGACTCCAGCCACCGTGGCCACTGGAGAC	13187	QY	3218	TCCTCAGGCTGCCCTCTCCCACTTCACTCAGTTCCCAAAATCTAAATTTTACAGAGA	3277
QY	2138	CTCAGGCCAGTGTGTACCTCCAGCTCCAGCTCTCAAGTCTGTAATAGGAGTTGCATTCCTAC	2197	Db	14268	TCCTCAGGCTGCCCTCTCCCACTTCACTCAGTTCCCAAAATCTAAATTTTACAGAGA	14327
Db	13188	CTCAGGCCAGTGTGTGTACCTCCAGCTCCAGCTCTCAAGTCTGTAATAGGAGTTGCATTCCTAC	13247	QY	3278	TTCTGTTTGGGGAACCTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAAT	3337
QY	2198	TTCTTAAATCTCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGAGATACAGCT	2257	Db	14328	TTCTGTTTGGGGAACCTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAAT	14387
Db	13248	TTCTTAAATCTCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGAGATACAGCT	13307	QY	3338	GTCAATTTCCCTAGAGAAAGTTAGGTTGGTGGAGCAAGCCCACTGGCTTTTCTGCC	3397
QY	2258	TTGATCCAGAGTGTGACATGGCTTCTCCTCAGGGCAACCCCTGCCCAACCCCTCATCCCC	2317	Db	14388	GTCAATTTCCCTAGAGAAAGTTAGGTTGGTGGAGCAAGCCCACTGGCTTTTCTGCC	14447
Db	13308	TTGATCCAGAGTGTGACATGGCTTCTCCTCAGGGCAACCCCTGCCCAACCCCTCATCCCC	13367	QY	3398	ACAGCATCCAATCGTGAAGAACTCGGAGAGGTTGGAGTCCACATCTAGGGTTGTCTGC	3457
QY	2318	ATCTTCTCAGGGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA	2377	Db	14448	ACAGCATCCAATCGTGAAGAACTCGGAGAGGTTGGAGTCCACATCTAGGGTTGTCTGC	14507
Db	13368	ATCTTCTCAGGGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA	13427	QY	3458	CCCTTGGCTCTATCCCTGCCAGAGGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGCC	3517
QY	2378	GGAACTGTACAGCATGGCCAGTATGGCAGCCCGGAAAGACACAGCACCCCTCTTATG	2437	Db	14508	CCCTTGGCTCTATCCCTGCCAGAGGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGCC	14567
Db	13428	GGAACTGTACAGCATGGCCAGTATGGCAGCCCGGAAAGACACAGCACCCCTCTTATG	13487	QY	3518	TAAATGTTCCCGGCTTGCATTTTCTTCTAGTCTCTGGGGCTAGATTTCTGCATTTGG	3577
QY	2438	TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTATGGGCCATTTACCCCTTGACCCC	2497	Db	14568	TAAATGTTCCCGGCTTGCATTTTCTTCTAGTCTCTGGGGCTAGATTTCTGCATTTGG	14627
Db	13488	TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTATGGGCCATTTACCCCTTGACCCC	13547	QY	3578	GGTCTCTGACACAACACACCATCCCAAGTAGCCGGAAGAGCTTAAACACAGGGGGTCTT	3637
QY	2498	AGTCCACAGTGTACAGGTAAGTACCTGGTCTTAGGGTTGCTCAGAGCCCAACCTCTCCT	2557	Db	14628	GGTCTCTGACACAACACACCATCCCAAGTAGCCGGAAGAGCTTAAACACAGGGGGTCTT	14687
Db	13548	AGTCCACAGTGTACAGGTAAGTACCTGGTCTTAGGGTTGCTCAGAGCCCAACCTCTCCT	13607	QY	3638	AAAATGGTGGCCCGGCAACCCGGGCTCCCTTGGGCAAAAGAAATTTGTTCAGCCCTAGCC	3697
QY	2558	GCCACCCCAACACCAAGAACTATATGTTTCTTCTTCCCACTGATCTGCTGGTCAATG	2617	Db	14688	AAAATGGTGGCCCGGCAACCCGGGCTCCCTTGGGCAAAAGAAATTTGTTCAGCCCTAGCC	14747
Db	13608	GCCACCCCAACACCAAGAACTATATGTTTCTTCTTCCCACTGATCTGCTGGTCAATG	13667	QY	3698	CAACCCCTCAACTACCAGAACTCTGGGCCACCCAGCAGTATTTTATTTTAAATTTGCC	3757
QY	2618	ATGATGCTGGCTGTGGAGGACCTGTGTAGTTGAGTCCACACATTAATATAGTCAATGTC	2677	Db	14748	CAACCCCTCAACTACCAGAACTCTGGGCCACCCAGCAGTATTTTATTTTAAATTTGCC	14807
Db	13668	ATGATGCTGGCTGTGGAGGACCTGTGTAGTTGAGTCCACACATTAATATAGTCAATGTC	13727	QY	3758	CATTTTATGATGATGATCAATTTGTATTAAATTAAGCTTACAGATGTCA	3807
QY	2678	CACCACTTCTTCCCAACAGCCGAGGAGACAGGGTGAAGGATATACCAAGCTGATGAC	2737	Db	14808	CATTTTATGATGATGATCAATTTGTATTAAATTAAGCTTACAGATGTCA	14857
Db	13728	CACCACTTCTTCCCAACAGCCGAGGAGACAGGGTGAAGGATATACCAAGCTGATGAC	13787				
QY	2738	AGCCCATTAGCCTAAAGCAACTGCAGGACAGCCCTCCCTGGATGATCGAGGTCCCCAGT	2797				

US-09-927-091-8		Query Match		53.2%; Score 2037; DB 9; Length 30676;	
; Sequence 8, Application US/09927091		Best Local Similarity		99.9%; Pred. No. 0;	
; Patent No. US20020119541A1		Matches 2327; Conservative		0; Mismatches 1; Indels 2; Gaps 2;	
; GENERAL INFORMATION:					
; APPLICANT: KILLARY, ANN					
; APPLICANT: LOTT, STEVE					
; APPLICANT: CHANDLER, DAWN					
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1					
; FILE REFERENCE: UTS:651US					
; CURRENT APPLICATION NUMBER: US/09/927,091					
; CURRENT FILING DATE: 2001-08-09					
; PRIOR APPLICATION NUMBER: 60/227,560					
; PRIOR FILING DATE: 2000-08-23					
; PRIOR APPLICATION NUMBER: 60/225,033					
; PRIOR FILING DATE: 2000-08-10					
; NUMBER OF SEQ ID NOS: 9					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 8					
; LENGTH: 30676					
; TYPE: DNA					
; ORGANISM: Human					
; FEATURE:					
; NAME/KEY: modified base					
; LOCATION: (667)..(30676)					
; OTHER INFORMATION: n = A or C or G or T/U					
US-09-927-091-8					
QY	1478	CAGTGCAGCGCGCCCTAACCTGGACCGCGGACAGCCACAGCGCCTGATCTCTGCGG	1537		
DB	23420	CAGTGCAGCGCGCCCTAACCTGGACCGCGGACAGCCACAGCGCCTGATCTCTGCGG	23479		
QY	1538	ACGACTGCACCATGTGGCTTACGGCAACTTGGACCCACAGCCACTCGAGACTCGCCAA	1597		
DB	23480	ACGACTGCACCATGTGGCTTACGGCAACTTGGACCCACAGCCACTCGAGACTCGCCAA	23539		
QY	1598	AGCGCTTCGATGTGGAGGTGTGGTGTCTGAGCTTCTGAAGCTTCTAGTAGTGGCGTCCACT	1657		
DB	23540	AGCGCTTCGATGTGGAGGTGTGGTGTCTGAGCTTCTGAAGCTTCTAGTAGTGGCGTCCACT	23599		
QY	1658	ACTGGCAGGTGTGTGGCGGAGACACCCAGTGGTGTGATCGGCTGGCACAGAGCCG	1717		
DB	23600	ACTGGCAGGTGTGTGGCGGAGACACCCAGTGGTGTGATCGGCTGGCACAGAGCCG	23659		
QY	1718	CAAGCCGCAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGCACTCGTGATGC	1777		
DB	23660	CAAGCCGCAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGCACTCGTGATGC	23718		
QY	1778	ACGATGGCAACCACTAGTACAGCGCTGCAAGGAGCCAGTGGTGTGATCGGCTGGCACAGAGCCG	1837		
DB	23719	ACGATGGCAACCACTAGTACAGCGCTGCAAGGAGCCAGTGGTGTGATCGGCTGGCACAGAGCCG	23778		
QY	1838	AGCTTTGACAAGTGGGTGTCTTCTTGGACTATGACCAAGGCTTGTCTCATCTTCTACAAATG	1897		
DB	23779	AGCTTTGACAAGTGGGTGTCTTCTTGGACTATGACCAAGGCTTGTCTCATCTTCTACAAATG	23838		
QY	1898	CTGATGACATGTCCTGGCTCTACACCTTCGGGAGAGTTCCTCGCAAGCTCTGTCTCTT	1957		
DB	23839	CTGATGACATGTCCTGGCTCTACACCTTCGGGAGAGTTCCTCGCAAGCTCTGTCTCTT	23898		
QY	1958	ACTTCAGCCCTGGCCAGAGCCACGCCAATGGCAAGAGTTTCAGCCGCTGCGGATCAACA	2017		
DB	23899	ACTTCAGCCCTGGCCAGAGCCACGCCAATGGCAAGAGTTTCAGCCGCTGCGGATCAACA	23958		
QY	2018	CGTTCGCACTTAGTCCAGGAGAGGAGACCAACCTCTCTGGGACCACTGCCACCTGC	2077		
DB	23959	CGTTCGCACTTAGTCCAGGAGAGGAGACCAACCTCTCTGGGACCACTGCCACCTGC	24018		
QY	2078	AAGAGCCCTGCCAGGAAGATAGAGACTTGGAACTCCAGCCCAAGCTGGCCACTGGAGAC	2137		

QY	3218	TCCGTGAGGCCTGCCCTCTCCCACTTCACTCAGTTCCCAAATCTAAATTTTACAAGAGA	3277
Db	25158	TCCGTGAGGCCTGCCCTCTCCCACTTCACTCAGTTCCCAAATCTAAATTTTACAAGAGA	25217
QY	3278	TTCTGTTTTGGGGAACTTAAGTCAGATCCAGAACCTTGCGTCGAAGGAGTCTGGGAAAT	3337
Db	25218	TTCTGTTTTGGGGAACTTTAAGTCAGATCCAGAACCTTGCGTCGAAGGAGTCTGGGAAAT	25277
QY	3338	GTCAATTTCCTAGAGGAACTTAGGTGAGTGAGGCAAGCCCCACCTGGGTTTTCTGCC	3397
Db	25278	GTCAATTTCCTAGAGGAACTTAGGTGAGTGAGGCAAGCCCCACCTGGGTTTTCTGCC	25337
QY	3398	ACAGCATCCAATCGTGAAGAACTCGGGAGAGGCTGAGTCCACATCTAGGGTTGTCCCTGC	3457
Db	25338	ACAGCATCCAATCGTGAAGAACTCGGGAGAGGCTGAGTCCACATCTAGGGTTGTCCCTGC	25397
QY	3458	CCCTTGGCTCTATCCCTGCCAGAGGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGCC	3517
Db	25398	CCCTTGGCTCTATCCCTGCCAGAGGTGGGAACTGGAGGAGTGGGCTGCAAGACTGAGCC	25457
QY	3518	TAAATGTCTCCCGGCTTGACATTTCTTCTAGTCTCTGGGCTTAGATTTCTGCACTTGG	3577
Db	25458	TAAATGTCTCCCGGCTTGACATTTCTTCTAGTCTCTGGGCTTAGATTTCTGCACTTGG	25517
QY	3578	GGTCTCTGACACACACACATCCCAAGTAGCCGGAAGAGCTAAAAACAAGGGGTTCTT	3637
Db	25518	GGTCTCTGACACACACACATCCCAAGTAGCCGGAAGAGCTAAAAACAAGGGGTTCTT	25577
QY	3638	AAAATGGCTGCCCGGCCACACCGCGGCTTCCCTTGGGCAAAAGGAAATGTTCAGCCCTACCC	3697
Db	25578	AAAATGGCTGCCCGGCCACACCGCGGCTTCCCTTGGGCAAAAGGAAATGTTCAGCCCTACCC	25637
QY	3698	CAACCCCTTCAACTACCAGAACTCTGGGCCACCCAGAGAGTATTTTATTTAAATGTGGC	3757
Db	25638	CAACCCCTTCAACTACCAGAACTCTGGGCCACCCAGAGAGTATTTTATTTAAATGTGGC	25697
QY	3758	CATTTATGAGTTATGATCAATTTCTATTAAATTTAAAGTTACAGATGTCA	3807
Db	25698	CATTTATGAGTTATGATCAATTTCTATTAAATTTAAAGTTACAGATGTCA	25747
RESULT 4			
US-09-927-091-5			
; Sequence 5, Application US/09927091			
; Patent No. US20020119541A1			
; GENERAL INFORMATION:			
; APPLICANT: KILLARY, ANN			
; APPLICANT: CHANDLER, DAWN			
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1			
; FILE REFERENCE: UTSC:651US			
; CURRENT APPLICATION NUMBER: US/09/927,091			
; CURRENT FILING DATE: 2001-08-09			
; PRIOR APPLICATION NUMBER: 60/227,560			
; PRIOR FILING DATE: 2000-08-23			
; PRIOR APPLICATION NUMBER: 60/225,033			
; PRIOR FILING DATE: 2000-08-10			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 5			
; LENGTH: 30625			
; TYPE: DNA			
; ORGANISM: Human			
; FEATURE:			
; NAME/KEY: modified base			
; LOCATION: (4754) ..(30625)			
; OTHER INFORMATION: n = A or C or G or T/U			
US-09-927-091-5			
Query Match			
24.3%; Score 928; DB 9; Length 30625;			

Query Match 24.3%; Score 928; DB 9; Length 30625;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 3227 CTGCCCTCTCCACTTCACTCAGTTCCTCCAAATCTAAATTTTCAAGAGATTCCTGTTG 3286
Db |||||
QY 23703 CTGCCCTCTCCACTTCACTCAGTTCCTCCAAATCTAAATTTTCAAGAGATTCCTGTTG 23762
Db |||||
QY 3287 GGGAACTTAAGTCAGATCCAGACTTGGTGCAGGGAGTCTGGGAAATGTCAATTTCC 3346
Db |||||
QY 23763 GGGAACTTAAGTCAGATCCAGAACTTGGTGCAGGGAGTCTGGGAAATGTCAATTTCC 23822
Db |||||
QY 3347 CTAGAAGAACTTAAGTGGGTGGAGCAAGCCACCTGCCTGCTTTTCTGCCACAGCATCC 3406
Db |||||
QY 23823 CTAGAAGAACTTAAGTGGGTGGAGCAAGCCACCTGCCTGCTTTTCTGCCACAGCATCC 23882
Db |||||
QY 3407 AATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTGTCTGCTGCCCTTGGCT 3466
Db |||||
QY 23883 AATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTGTCTGCTGCCCTTGGCT 23942
Db |||||
QY 3467 CTATCCCTGCCACAGGTGGAACTGGAGAGTGGCTGCAAGACTGAGCCTAAATGTCT 3526
Db |||||
QY 23943 CTATCCCTGCCACAGGTGGAACTGGAGAGTGGCTGCAAGACTGAGCCTAAATGTCT 24002
Db |||||
QY 3527 CCCGGGCTTGAATTTCTTTCTAGTCTCGGGCTAGATTTCTGCACTTGGGGTCTCTGA 3586
Db |||||
QY 24003 CCCGGGCTTGAATTTCTTTCTAGTCTCGGGCTAGATTTCTGCACTTGGGGTCTCTGA 24062
Db |||||
QY 3587 CACAACACCATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCT 3646
Db |||||
QY 24063 CACAACACCATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCT 24122
Db |||||
QY 3647 GCCCGCCACCCGGGCTCTCTGGGCAAGAAAGTGTGAGCCTTACCCCAACCCCTTC 3706
Db |||||
QY 24123 GCCCGCCACCCGGGCTCTCTGGGCAAGAAAGTGTGAGCCTTACCCCAACCCCTTC 24182
Db |||||
QY 3707 AACTACAGAACTCTGGCCACCCAGCAGTATTTTAAATGTTGAGGCTTTTATG 3766
Db |||||
QY 24183 AACTACAGAACTCTGGCCACCCAGCAGTATTTTAAATGTTGAGGCTTTTATG 24242
Db |||||
QY 3767 AGTTATGATCAATTTGTATTAATTAAGTTACAGATGTCA 3807
Db |||||
QY 24243 AGTTATGATCAATTTGTATTAATTAAGTTACAGATGTCA 24283
Db |||||

RESULT 5

US-09-927-091-6
; Sequence 6, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 45845
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-6

Query Match 20.6%; Score 788; DB 9; Length 45845;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1008; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 AGGCTGCGCTGGAACCAAGCGGTGCTGCTAGCTCGCGGGTAAGGGGTGCGCTGGG 60
Db |||||
24164 AGGCTGCGCTGGAACCAAGCGGTGCTGCTAGCTCGCGGGTAAGGGGTGCGCTGGG 24223
Db |||||

QY 61 CCAGGGTTTGGGGCGGGATCCGGCAGCTGAGCGGCGCGACCCCTCTCTCTCTCTGCC 120
Db |||||
24224 CCAGGGTTTGGGGCGGGATCCGGCAGCTGAGCGGCGCGACCCCTCTCTCTCTGCC 24283
QY 121 GGTACACAGCAATCTAGCGCTCGGCTGCGCTCCCTCCCTCCAGGATTCGCCATCCCA 180
Db |||||
24284 GGTACACAGCAATCTAGCGCTCGGCTGCGCTCCCTCCCTCCAGGATTCGCCATCCCA 24343
QY 181 GTTCTTCGCTCCCTCCCGCACCGCCCGGATTTTCAGCCCTTTCAGAGGCTCCAC 240
Db |||||
24344 GTTCTTCGCTCCCTCCCGCACCGCCCGGATTTTCAGCCCTTTCAGAGGCTCCAC 24403
QY 241 CCCGCTCGGGATCCCTTCTCCAGCTCTTATCCCTTAGGACTGCCCCGCCCTAGAA 300
Db |||||
24404 CCCGCTCGGGATCCCTTCTCCAGCTCTTATCCCTTAGGACTGCCCCGCCCTAGAA 24463
QY 301 CTTCCCGCTCAGGATCTCCGCTCCTCAGCGCTCAGAGCTCTCCAGAGCGCATGCCC 360
Db |||||
24464 CTTCCCGCTCAGGATCTCCGCTCCTCAGCGCTCAGAGCTCTCCAGAGCGCATGCCC 24523
QY 361 TTGAGCTGCCCACTTACCTCTAGACTGCCCTCCCGGGTGGCGTCCACGAGTCTCAGCC 420
Db |||||
24524 TTGAGCTGCCCACTTACCTCTAGACTGCCCTCCCGGGTGGCGTCCACGAGTCTCAGCC 24583
QY 421 GCGACCCCTTCTCTGCGGTTCCTTCCGACAGCACCCCTCTCTCTCGGTAGC 480
Db |||||
24584 GCGACCCCTTCTCTGCGGTTCCTTCCGACAGCACCCCTCTCTCTCGGTAGC 24643
QY 481 TCTTACCCCTGCTGTGGGGCTCTGCTCCCGGGCCAGCCCTCGGTGCTCGGATCGGACA 540
Db |||||
24644 TCTTACCCCTGCTGTGGGGCTCTGCTCCCGGGCCAGCCCTCGGTGCTCGGATCGGACA 24703
QY 541 GCGCGCGCTCTCTCAGCGCGCCCTCTGCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 600
Db |||||
24704 GCGCGCGCTCTCTCAGCGCGCCCTCTGCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 24762
QY 601 GCCATGGGTGACGCTCAAGGACGAGTCTGCTGCTCCATCTGCTGAGCATCTTACCAG 660
Db |||||
24763 GCCATGGGTGACGCTCAAGGACGAGTCTGCTGCTCCATCTGCTGAGCATCTTACCAG 24822
QY 661 GACCCGCTGAGCTGCGGCTGCGGACACTTCTGCGCGCTGCGATCAGGAGCATGCG 720
Db |||||
24823 GACCCGCTGAGCTGCGGCTGCGGACACTTCTGCGCGCTGCGATCAGGAGCATGCG 24882
QY 721 GTGCGCAGGAGCGCAGGGCGCCCGGACTGCGCGAGTGGCGGCGACGTTTCGCGGAG 780
Db |||||
24883 GTGCGCAGGAGCGCAGGGCGCCCGGACTGCGCGAGTGGCGGCGACGTTTCGCGGAG 24942
QY 781 CCGCGCTGCGGCGCAGCTCAAGCTGCGCAACATCTGCGAGCGCTTACAGCTCTTCCCG 840
Db |||||
24943 CCGCGCTGCGGCGCAGCTCAAGCTGCGCAACATCTGCGAGCGCTTACAGCTCTTCCCG 25002
QY 841 CTGAGAGCCCATCTCAAACGCGCGCGCGCGGACCTGCGAGCGCGCAGCAAGGTC 900
Db |||||
25003 CTGAGAGCCCATCTCAAACGCGCGCGCGCGGACCTGCGAGCGCGCAGCAAGGTC 25062
QY 901 AAGCTCTTCTGCTCAGGACCGCGGCTTCTCTGCTTCTCTGCGAGCGCTGCGACTG 960
Db |||||
25063 AAGCTCTTCTGCTCAGGACCGCGGCTTCTCTGCTTCTCTGCGAGCGCTGCGACTG 25122
QY 961 CACGAGCAGCATCAGGTACCGGCTACGAGCGCTTTCGAGAGCTGCGAG 1011
Db |||||
25123 CACGAGCAGCATCAGGTACCGGCTACGAGCGCTTTCGAGAGCTGCGAG 25173
Db |||||

RESULT 6

US-10-027-632-100265/c
; Sequence 100265, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome

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; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100265
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-100265

Query Match      15.0%; Score 575; DB 16; Length 610;
Best Local Similarity 100.0%; Pred. No. 5.6e-274;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345 CCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTCCAGAGCATGGCCAGTAGTT 2404
DB 610 CCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTCCAGAGCATGGCCAGTAGTT 551
QY 2405 GGCAGCCGGAAGACACACAGCACCCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 2464
DB 550 GGCAGCCGGAAGACACACAGCACCCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 491
QY 2465 CAAGCTAGTGTGGGCCATTTACCCCTTGACCCAGTCCACAGTGTGTACAGTAGTACCT 2524
DB 490 CAAGCTAGTGTGGGCCATTTACCCCTTGACCCAGTCCACAGTGTGTACAGTAGTACCT 431
QY 2525 GGTCTAGGTTGCTTCAGAGCAACCTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 2584
DB 430 GGTCTAGGTTGCTTCAGAGCAACCTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 371
QY 2585 TTCTCTACTTCTCCCACTGATCTGCTGGTCAAGTGTGATGCTGTGGCTGTGGAAGCACC 2644
DB 370 TTCTCTACTTCTCCCACTGATCTGCTGGTCAAGTGTGATGCTGTGGCTGTGGAAGCACC 311
QY 2645 TGGTAGTTGAGTCCACACATTATAGTCAATGTCATGTCGACCACTTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 2704
DB 310 TGGTAGTTGAGTCCACACATTATAGTCAATGTCATGTCGACCACTTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 251
QY 2705 GACAGGTTGAGGTATACCCAAAGCTGATGTCAGAGCCCAATAGCTTAAAGCAACTATGCGAG 2764
DB 250 GACAGGTTGAGGTATACCCAAAGCTGATGTCAGAGCCCAATAGCTTAAAGCAACTATGCGAG 191
QY 2765 GACAAAGCTCCCTGGATGATCGAGGTCCCAGTAGTCTTGAAACAAGAGTCCAGCCAAACC 2824
DB 190 GACAAAGCTCCCTGGATGATCGAGGTCCCAGTAGTCTTGAAACAAGAGTCCAGCCAAACC 131
QY 2825 TCTTCAGCCAGGCTCTGTGACCTGTAGGTCAGAGGCTTCCAGAGCAGTGTGTGT 2884
DB 130 TCTTCAGCCAGGCTCTGTGACCTGTAGGTCAGAGGCTTCCAGAGCAGTGTGTGT 71
QY 2885 AATTAGACCCAAAGCACTGGAGGGGCTGTGTGGCT 2919
DB 70 AATTAGACCCAAAGCACTGGAGGGGCTGTGTGGCT 36

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; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100265
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-100265

Query Match      15.0%; Score 575; DB 13; Length 610;
Best Local Similarity 100.0%; Pred. No. 5.6e-274;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345 CCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTCCAGAGCATGGCCAGTAGTT 2404
DB 610 CCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTCCAGAGCATGGCCAGTAGTT 551
QY 2405 GGCAGCCGGAAGACACACAGCACCCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 2464
DB 550 GGCAGCCGGAAGACACACAGCACCCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 491
QY 2465 CAAGCTAGTGTGGGCCATTTACCCCTTGACCCAGTCCACAGTGTGTACAGTAGTACCT 2524
DB 490 CAAGCTAGTGTGGGCCATTTACCCCTTGACCCAGTCCACAGTGTGTACAGTAGTACCT 431
QY 2525 GGTCTAGGTTGCTTCAGAGCAACCTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 2584
DB 430 GGTCTAGGTTGCTTCAGAGCAACCTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 371
QY 2585 TTCTCTACTTCTCCCACTGATCTGCTGGTCAAGTGTGATGCTGTGGCTGTGGAAGCACC 2644
DB 370 TTCTCTACTTCTCCCACTGATCTGCTGGTCAAGTGTGATGCTGTGGCTGTGGAAGCACC 311
QY 2645 TGGTAGTTGAGTCCACACATTATAGTCAATGTCATGTCGACCACTTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 2704
DB 310 TGGTAGTTGAGTCCACACATTATAGTCAATGTCATGTCGACCACTTCTCTGCGCAGCCACCTCTTATGTCCTTCCATGGCTTAAGACTTACCCCTGAC 251
QY 2705 GACAGGTTGAGGTATACCCAAAGCTGATGTCAGAGCCCAATAGCTTAAAGCAACTATGCGAG 2764
DB 250 GACAGGTTGAGGTATACCCAAAGCTGATGTCAGAGCCCAATAGCTTAAAGCAACTATGCGAG 191
QY 2765 GACAAAGCTCCCTGGATGATCGAGGTCCCAGTAGTCTTGAAACAAGAGTCCAGCCAAACC 2824
DB 190 GACAAAGCTCCCTGGATGATCGAGGTCCCAGTAGTCTTGAAACAAGAGTCCAGCCAAACC 131
QY 2825 TCTTCAGCCAGGCTCTGTGACCTGTAGGTCAGAGGCTTCCAGAGCAGTGTGTGT 2884
DB 130 TCTTCAGCCAGGCTCTGTGACCTGTAGGTCAGAGGCTTCCAGAGCAGTGTGTGT 71
QY 2885 AATTAGACCCAAAGCACTGGAGGGGCTGTGTGGCT 2919
DB 70 AATTAGACCCAAAGCACTGGAGGGGCTGTGTGGCT 36

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RESULT 7

US-10-027-632-100265/c

; Sequence 100265, Application US/10027632

RESULT 8
US-09-864-761-7231/c
; Sequence 7231, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 7231
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC02262.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
US-09-864-761-7231

Query Match 12.9%; Score 493; DB 9; Length 573;
Best Local Similarity 100.0%; Pred. No. 2.4e-233;
Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1602	CTTCGATGTGAGGTGTTCGGTCTGAGGCTTCTAGTGTGGGTCCACTACTG	1661
DB	573	CTTCGATGTGAGGTGTTCGGTCTGAGGCTTCTAGTGTGGGTCCACTACTG	514
QY	1662	GGAGTGTGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCACGAGCGCAAG	1721
DB	513	GGAGTGTGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCACGAGCGCAAG	454
QY	1722	CCGAAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGTCATCGTATCAGCA	1781
DB	453	CCGAAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGTCATCGTATCAGCA	394
QY	1782	TGGCAACCAGTACACGCGCTTCGACGAGCCCTTGACGCGGCTTAACTGTCGCGGACAAGCT	1841
DB	393	TGGCAACCAGTACACGCGCTTCGACGAGCCCTTGACGCGGCTTAACTGTCGCGGACAAGCT	334
QY	1842	TGCAAGGTGGGTGTCTTCCTGGACTATGACCAAGGCTTGTCTATCTTCTACAATGCTGA	1901
DB	333	TGCAAGGTGGGTGTCTTCCTGGACTATGACCAAGGCTTGTCTATCTTCTACAATGCTGA	274
QY	1902	TGACATGTCTCTGGCTCTACACCTTCCGCGAGAGTTCCTTGGCAAGCTTCCCTGCGAAGCTT	1961
DB	273	TGACATGTCTCTGGCTCTACACCTTCCGCGAGAGTTCCTTGGCAAGCTTCCCTGCGAAGCTT	214
QY	1962	CAGCCCTGGCGAGAGCCACCCCAATGCAAGAGAGCTTTCAGCCGCTGCGGATCAACACCGT	2021
DB	213	CAGCCCTGGCGAGAGCCACCCCAATGCAAGAGAGCTTTCAGCCGCTGCGGATCAACACCGT	154
QY	2022	CCGATCTAGTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2081
DB	153	CCGATCTAGTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	94
QY	2082	GCCTTGCCCGAGGA 2094	
DB	93	GCCTTGCCCGAGGA 81	

RESULT 9

US-09-864-761-23962/c
; Sequence 23962, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

	Query Match	11.3%	Score 431	DB 9	Length 431	
	Best Local Similarity	100.0%	Prod. No. 1.3e-202			
	Matches 431	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1643	GTAGTGGCGTCCACTACTCTGGGAGGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGC	1702			
Db	431	GTAGTGGCGTCCACTACTCTGGGAGGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGC	372			
QY	1703	TGGCACACGAAGCGCGAAGCGCAAGGCGAGCATCCAGATCCAGCCAGCGCGGGCTTCT	1762			
Db	371	TGGCACACGAAGCGCGAAGCGCGAAGGCGAGCATCCAGATCCAGCCAGCGCGGGCTTCT	312			
QY	1763	ACTGCATCTGATGCAGCATGGCAACAGATACAGCGCTGCACGGAGCCCTGACGCGGC	1822			
Db	311	ACTGCATCTGATGCAGCATGGCAACAGATACAGCGCTGCACGGAGCCCTGACGCGGC	252			
QY	1823	TTAAGTCGGGACAGCTTGACAAAGTGGGTGTCTTCCTGGACTATGACCAAGGCTTG	1882			
Db	251	TTAAGTCGGGACAGCTTGACAAAGTGGGTGTCTTCCTGGACTATGACCAAGGCTTG	192			
QY	1893	TCATCTTCTCAATGCTGATGACATGTCTGGCTCTACACCTTCCGGAGAGTTCCCTG	1942			
Db	191	TCATCTTCTCAATGCTGATGACATGTCTGGCTCTACACCTTCCGGAGAGTTCCCTG	132			
QY	1943	GCAAGCTGTGCTTTACTTTAGCCCTGGCGAGCCAGCCCAATGGCGAAGACGTTGACG	2002			
Db	131	GCAAGCTGTGCTTTACTTTAGCCCTGGCGAGCCAGCCCAATGGCGAAGACGTTGACG	72			
QY	2003	CGCTGGGATCAACACCGTCCGCATCTAGTCAGGCGAAGGAGACCAACACCTCCTGGG	2062			
Db	71	CGCTGGGATCAACACCGTCCGCATCTAGTCAGGCGAAGGAGACCAACACCTCCTGGG	12			
QY	2063	ACCATGCGAC	2073			
Db	11	ACCATGCGAC	1			

RESULT 11

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RESULT 11
US-09-908-975-16197
; Sequence 16197, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16197
; LENGTH: 60
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-908-975-16197

Query Match
Best Local Similarity 1.6%; Score 60; DB 10; Length 60;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3668 CTTGGGCAAAAGGAATTGTGAGCCCTTACCCCAACCTTCACTACCAAGATCTGGGCCAC 3727
Db 1 CTTGGGCAAAAGGAATTGTGAGCCCTTACCCCAACCTTCACTACCAAGATCTGGGCCAC 60

RESULT 12
US-10-116-275-299/c
; Sequence 299, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Eian Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 299
; LENGTH: 1652
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-275-299

Query Match
Best Local Similarity 0.8%; Score 29; DB 16; Length 1652;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3798 ACAGATGTCACAAAAAATAAAAAAAAAAAAAA 3826
Db 1474 ACAGATGTCACAAAAAATAAAAAAAAAAAAAA 1446

RESULT 13
US-10-437-963-80513
; Sequence 80513, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80513
; LENGTH: 1754
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80128C.1
US-10-437-963-80513

Query Match
Best Local Similarity 0.7%; Score 27; DB 17; Length 1754;
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; Sequence 27, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2014
; LENGTH: 248436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(248436)
; OTHER INFORMATION: n = A, T, C or G
US-10-087-192-2014
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Best Local Similarity 0.7%; Score 27; DB 13; Length 248436;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3800 AGATGTCACAAAAAATAAAAAAAAAAAAAA 3826
Db 187916 AGATGTCACAAAAAATAAAAAAAAAAAAAA 187890
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RESULT 15
US-09-969-034-4195
; Sequence 4195, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4195
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-034-4195
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us-09-927-091-3.oli15.rnpb

Mon Aug 2 10:03:35 2004

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 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3801 GATGTCAAAAAAAAAAAAAAAAAAAAA 3826
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 DB 245 GATGTCAAAAAAAAAAAAAAAAAAAAA 270

Search completed: July 31, 2004, 12:31:55
 Job time : 1604 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 01:26:32 ; Search time 9090 seconds
(without alignments)
12569.054 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggtgtgctggaccgaagc.....aaaaaaaaaaaaaaaaaaaaa 3826

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 15

Total number of hits satisfying chosen parameters: 2492743

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: em_estba:*

2: em_esthum:*

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5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	721	18.8	769	14	CA444761
4	656	17.1	781	14	CB956370

5	647	16.9	785	14	CB960090
6	634	16.6	634	12	BQ018441
7	634	16.6	935	13	BQ069145
8	632	16.5	632	12	BM994555
9	617	16.1	841	14	CF995034
10	613	16.0	664	12	BM722392
11	594	15.5	851	12	BM703589
12	594	15.5	931	13	BU527114
13	587	15.3	682	14	CA309985
14	582	15.2	633	12	BM994326
15	533	13.9	628	9	AU132503
16	519	13.6	519	9	AL138362
17	509	13.3	510	13	BM283437
18	508	13.3	973	13	BQ879837
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21	455	11.9	470	10	AW515028
22	441	11.5	868	13	BQ069935
23	440	11.5	486	9	AI457621
24	434	11.3	451	14	CA434008
25	431	11.3	477	10	BE671191
26	427	11.2	705	10	BE258134
27	423	11.1	557	9	AU154016
28	421	11.0	423	9	AI066431
29	421	11.0	501	13	BQ187235
30	415	10.8	983	10	BE795637
31	405	10.6	456	10	BE856182
32	403	10.5	456	9	AA700789
33	399	10.4	502	14	CK300567
34	391	10.2	512	9	AI681374
35	386	10.1	507	10	BE115402
36	378	9.9	431	14	R71654
37	370	9.7	497	10	BE244684
38	367	9.6	998	13	BU553767
39	337	8.8	810	14	CB960174
40	319	8.3	424	14	CA434086
41	317	8.3	906	13	BU171407
42	305	8.0	543	14	R71157
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44	299	7.8	376	10	BE245533
45	286	7.5	385	9	AA644653

ALIGNMENTS

RESULT 1
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM457033 1049 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.

BM457033

BM457033.1 GI:18506073

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1049)

NIH-MGC <http://mgc.hci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone Sequencing by: Agencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium information can be

<http://image.llnl.gov>

Plate: LLAM12346 row: b column: 06

High quality sequence stop: 671.

/tissue_type="Human Placenta"
 /lab_host="DH10B TonA"
 /clone_lib="NIH_MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site: 1:
 all-XhoI; Site: 2: BamH; Oligo-dr primed using primer
 5'-TTTTTTTTTTTTTTT-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

ORIGIN

Query Match 16.9%; Score 647; DB 14; Length 785;
 Best Local Similarity 99.9%; Pred. No. 8.4e-113;
 Matches 697; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 371 CACTACCTCTAGACTGCGCTCCCGGGTGGCGTCCACGGAGTCTCAGCCGCGCACCCCT 430
 Db 28 CACTACCTCTAGACTGCGCTCCCGGGTGGCGTCCACGGAGTCTCAGCCGCGCACCCCT 87

QY 431 TCCTCGCGTACCTCTCTCCGACAGACACCCCTCCCTCTCCGTTAGCTCTACCCCT 490
 Db 88 TCCTCGCGTACCTCTCTCCGACAGACACCCCTCCCTCTCCGTTAGCTCTACCCCT 147

QY 491 GCCTGTGCGGGCTCGTCCCGCGCCAGCCCTCGGTGCTGCTCCGACAGCGCGCGCT 550
 Db 148 GCCTGTGCGGGCTCGTCCCGCGCCAGCCCTCGGTGCTGCTCCGACAGCGCGCGCT 207

QY 551 CTCTAGCGCGCCCTCGTCCCGTGGGCCCCCTCTCTGCTGCGCCCTGGCGCCATGCGCT 610
 Db 208 CTCTAGCGCGCCCTCGTCCCGTGGGCCCCCTCTCTGCTGCGCCCTGGCGCCATGCGCT 267

QY 611 GCAGCTCTAAGGACGAGCTGCTGCTCATCTGCTGAGCATCTACGAGACCCGCTGA 670
 Db 268 GCAGCTCTAAGGACGAGCTGCTGCTCATCTGCTGAGCATCTACGAGACCCGCTGA 327

QY 671 GCCTGGCTGCGAGCACTACTTCTGCGCGCGTGCATCAGGAGCACTGGTGGCGCAGG 730
 Db 328 GCCTGGCTGCGAGCACTACTTCTGCGCGCGTGCATCAGGAGCACTGGTGGCGCAGG 387

QY 731 AGGCGAGGCGCGCGGAGTGCCTCGGCGCAGCTTTCGCGAGCCCGCGCTGG 790
 Db 388 AGGCGAGGCGCGCGGAGTGCCTCGGCGCAGCTTTCGCGAGCCCGCGCTGG 447

QY 791 CGCCCAAGCTCAAGCTGCGCAATCATGTCGAGCGCTACAGCTCTTCCGCTGGACGCA 850
 Db 448 CGCCCAAGCTCAAGCTGCGCAATCATGTCGAGCGCTACAGCTCTTCCGCTGGACGCA 507

QY 851 TCCTCAAGCGCGCGCGCGGCGGACCTTCCAGCGCGCACACAGGTCAAGCTCTTCT 910
 Db 508 TCCTCAAGCGCGCGCGCGGCGGACCTTCCAGCGCGCACACAGGTCAAGCTCTTCT 567

QY 911 GCCTCAGGACCGCGGCTTCTGCTTCTTCTGCGAGCGCTGCACTGCGAGCAGC 970
 Db 568 GCCTCAGGACCGCGGCTTCTGCTTCTTCTGCGAGCGCTGCACTGCGAGCAGC 627

QY 971 ATCAGCTCAGCGGCTCAGACGAGCTTCCGAGCTGCGAGGAGCTGAGGACCAAC 1030
 Db 628 ATCAGCTCAGCGGCTCAGACGAGCTTCCGAGCTGCGAGGAGCTGAGGACCAAC 687

QY 1031 TTCAGGCGCTTCAAGACGCGAGCGGGAACACACCGAA 1068
 Db 688 TTCAGGCGCTTCAAGACGCGAGCGGGAACACACCGAA 725

RESULT 6

BQ018441/c
 LOCUS
 DEFINITION BQ018441
 IMAGE:5893122 3', mRNA sequence.
 ACCESSION BQ018441

BQ018441.1 GI:19753718
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 634)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..634
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5893122"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP DH1"
 /note="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP DH1 is a normalized cDNA library containing the
 following tissue(s): VS-8 Cell line from Metastatic
 Chondrosarcoma in Lung. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dr primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into p77T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dr)18 tail. The
 sequence tag for this library is AGATCATTCG.
 TAG TISSUE=lung
 TAG LIB=UI-H-DH1
 TAG_SEQ=AGATCATTCG"

ORIGIN

Query Match 16.6%; Score 634; DB 12; Length 634;
 Best Local Similarity 100.0%; Pred. No. 2.8e-110;
 Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3191 GCCAGGTCGCGCCAGCAATAGATGCTGAGCGCTGCCCTCTCCACTCACTCAG 3250
 Db 634 GCCAGGTCGCGCCAGCAATAGATGCTGAGCGCTGCCCTCTCCACTCACTCAG 575

QY 3251 TTCCCAATCTAAATTTTACAGAGATTCTGTTGGGGGAACTTAAGTCAGATCCAGAA 3310
 Db 574 TTCCCAATCTAAATTTTACAGAGATTCTGTTGGGGGAACTTAAGTCAGATCCAGAA 515

QY 3311 CTTGGCTGCAAGGGAGTCTGGGAATGTCATTTCCCTAGAAGGAAGTTAGGGTGGGTGG 3370
 Db 514 CTTGGCTGCAAGGGAGTCTGGGAATGTCATTTCCCTAGAAGGAAGTTAGGGTGGGTGG 455

QY 3371 AGCAAGCCCACTCGCTTTTCTGCCACAGATCCAAATCGTGAAGAACTCGGGAGCGG 3430
 Db 454 AGCAAGCCCACTCGCTTTTCTGCCACAGATCCAAATCGTGAAGAACTCGGGAGCGG 395

QY 3431 TGGAGTCCACATCTAGGGTCTCTCGCCCTTGGCTCTATCCCTGCCAGAGGTGGGAAC 3490
 Db 394 TGGAGTCCACATCTAGGGTCTCTCGCCCTTGGCTCTATCCCTGCCAGAGGTGGGAAC 335

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..632
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5871536"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP DH0"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DH0 is a cDNA library containing the following
tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma
in lung. The library was constructed according to Bonaldo,
Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGATCATTCG.
TAG TISSUE=lung
TAG LIB=UI-H-DH0
TAG_SEQ=AGATCATTCG"

ORIGIN

Query Match 16.5%; Score 632; DB 12; Length 632;
Best Local Similarity 100.0%; Pred. No. 6.7e-110;
Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3193 CACGGTCCGTGCAGCAATAGATGTCCTCAGGCGCTGCCCTCTCCACCTTCACTCAGTT 3252
DB |||||
QY 632 CACGGTCCGTGCAGCAATAGATGTCCTCAGGCGCTGCCCTCTCCACCTTCACTCAGTT 573
DB |||||
QY 3253 CCCAATCTAAATTTTACAGAGATCTGTTGGGGAACTTAAGTCAGATCCAGAAC 3312
DB |||||
QY 572 CCCAATCTAAATTTTACAGAGATCTGTTGGGGAACTTAAGTCAGATCCAGAAC 513
DB |||||
QY 3313 TTGGCTCAAGGGAGTCTGGGAAATGTCATTTCCCTAGAGCAAGTATAGGTGGGTGGAG 3372
DB |||||
QY 512 TTGGCTCAAGGGAGTCTGGGAAATGTCATTTCCCTAGAGCAAGTATAGGTGGGTGGAG 453
DB |||||
QY 3373 CAAGCCCACTGCGTTTTCGCACAGCATCCCAATCGTGAAGAACTCGGAGAGGGTG 3432
DB |||||
QY 452 CAAGCCCACTGCGTTTTCGCACAGCATCCCAATCGTGAAGAACTCGGAGAGGGTG 393
DB |||||
QY 3433 GAGTCCACATCTAGGGTGTCTGCGCCCTTGCTCTATCCCTGCCAGAGGTGGAACTG 3492
DB |||||
QY 392 GAGTCCACATCTAGGGTGTCTGCGCCCTTGCTCTATCCCTGCCAGAGGTGGAACTG 333
DB |||||
QY 3493 GAGGAGTGGGTGCAAGACTGAGCCTAAATGTCCTCCGCGCTTGACCTTTCTTCTAGT 3552
DB |||||
QY 332 GAGGAGTGGGTGCAAGACTGAGCCTAAATGTCCTCCGCGCTTGACCTTTCTTCTAGT 273
DB |||||
QY 3553 CTTGGGCGCTAGATTCTGCACTTGGGGTCTCTGACACACACCATCCCAAGTAGCG 3612
DB |||||
QY 272 CTTGGGCGCTAGATTCTGCACTTGGGGTCTCTGACACACACCATCCCAAGTAGCG 213
DB |||||
QY 3613 GAAGAGCTAAACACAGGGGGTCTTAAATGGCTGCCCCGCCACCCCGGCGCTCCCTTGG 3672
DB |||||

Db

212 GAAGAGCTAAACACACAGGGGTCTTAAATGGCTGCCCGCCACCGGGCTCCCTTGG 153
QY |||||
3673 GCMAAAGGAATTTGTGAGCCCTACCCCAACCCCTTCAACTACGAGATCTGGGCGACCCAG 3732
DB |||||
152 GCMAAAGGAATTTGTGAGCCCTACCCCAACCCCTTCAACTACGAGATCTGGGCGACCCAG 93
QY |||||
3733 CAGTATTTTATTTTAAATTTGTTGCCCATTTATGATGATGATCAATTTGTATTAAATTA 3792
DB |||||
92 CAGTATTTTATTTTAAATTTGTTGCCCATTTATGATGATGATCAATTTGTATTAAATTA 33
QY |||||
3793 AAGTTACAGATGTCMAAATAAAAAA 3824
DB |||||
32 AAGTTACAGATGTCMAAATAAAAAA 1

RESULT 9

CF995034

LOCUS

CF995034

DEFINITION

CF995034

ACCESSION

CF995034

VERSION

CF995034.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 841)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM615 row: k column: 10
High quality sequence stop: 585.

FEATURES

Location/Qualifiers

1..841

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30528921"

/tissue_type="Human Placenta"

/lab_host="DH10B Tona"

/clone_lib="NIH MGC 147"

/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to 10⁶. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci,
preparation). Library constructed by M. Brownstein,
(NHGRI/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Query Match 16.1%; Score 617; DB 14; Length 841;
Best Local Similarity 100.0%; Pred. No. 3.4e-107;
Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCTGCGCTGGACCGAGCGGTGGCTGCTAAGCTCGGGGGTAAGGGGTGCGCTGGG 60
DB |||||

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES
source

Location/Qualifiers
1..664
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-E00-abx-d-01-0-UI"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-E00"
/notes="Organ: eye; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1; UI-E-E00 is a cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not 1 site. Double stranded cDNA was ligated to an EcoR 1 adaptor, digested with Not 1, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not 1 site and the (gt)18 tail. The sequence tag for this library is CCGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 16.0%; Score 613; DB 12; Length 664;
Best Local Similarity 99.8%; Pred. No. 2.4e-106;
Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
311 AGGATCTCCGTCCTCAGCGCTCCTCCAGCGCCATCGCTTGGTGGC 370
1 AGGATCTCCGTCCTCAGCGCTCCTCCAGCGCCATCGCTTGGTGGC 60
371 CACTACCTCTAGACTGCTCCCGGGCTGGGCTCCACGGAGTCTCAGCGGCGACCCCT 430
61 CACTACCTCTAGACTGCTCCCGGGCTGGGCTCCACGGAGTCTCAGCGGCGACCCCT 120
431 TCCTCGGTTACCTCTCCGAGCAGACCCCTCTCCGCTAGCTCTCAGCGGCGACCCCT 490
121 TCCTCGGTTACCTCTCCGAGCAGACCCCTCTCCGCTAGCTCTCAGCGGCGACCCCT 180
491 GCCTGTGGGGCTCTGTCCTCCCGCGCCAGCCCTCGGTGTGCTCCGAGCGCGCGCT 550
181 GCCTGTGGGGCTCTGTCCTCCCGCGCCAGCCCTCGGTGTGCTCCGAGCGCGCGCT 240
551 CTCTCAGCGCGCCCTCTGCTCCCGGGCTGGGCTCTCTGCTGCTCCCGCGCGCGCT 610
241 CTCTCAGCGCGCCCTCTGCTCCCGGGCTGGGCTCTCTGCTGCTCCCGCGCGCGCT 300
611 GCAGCTCTAAGAGCAGCTGCTGTGCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 670
301 GCAGCTCTAAGAGCAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
671 GCCTGTGGGGCTCTGCTGCTCCCGCGCCAGCCCTCGGTGTGCTCCGAGCGCGCGCT 730
361 GCCTGTGGGGCTCTGCTGCTCCCGCGCCAGCCCTCGGTGTGCTCCGAGCGCGCGCT 420
731 AGGCGCAGGCGCGCCCGAGTGTCCCGAGTGTCCCGAGTGTCCCGAGTGTCCCGAGTGT 790
421 AGGCGCAGGCGCGCCCGAGTGTCCCGAGTGTCCCGAGTGTCCCGAGTGTCCCGAGTGT 480
791 CGCCGAGCTCAAGCTGGCCCAACATCTGTGAGCGCTACAGCTCTCTCCCGCTGACGCCA 850
481 CGCCGAGCTCAAGCTGGCCCAACATCTGTGAGCGCTACAGCTCTCTCCCGCTGACGCCA 540
851 TCCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 910
541 TCCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

31 AGGCTGCGCTGACCGAGCGGTGGCTGTAAGCTCGCGGGGTAAGGGTTCGCGTGGG 90
61 CCAGGGTTTGGGCGCGGATCGGAGCTGAGCGGCGCGGACCCCTCTCTTCTGTGCC 120
91 CCAGGGTTTGGGCGCGGATCGGAGCTGAGCGGCGCGGACCCCTCTCTTCTGTGCC 150
121 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
151 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 210
181 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
211 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 270
241 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
271 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
301 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
331 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 390
361 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
391 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
421 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
451 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 510
481 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
511 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 570
541 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
571 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 630
601 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 617
631 GGTACAGCAATGTACGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 647

RESULT 10
BM722392
LOCUS
DEFINITION
UI-E-E00-abx-d-01-0-UI.r1 UI-E-E00 Homo sapiens cDNA clone
UI-E-E00-abx-d-01-0-UI 5', mRNA sequence.

BM722392 664 bp mRNA linear EST 01-MAR-2002
UI-E-E00-abx-d-01-0-UI.r1 UI-E-E00 Homo sapiens cDNA clone
UI-E-E00-abx-d-01-0-UI 5', mRNA sequence.
BM722392
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477

BM722392
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: benton-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

```

QY 911 GCCTCAGGACCGCGGCTTCTCTCTTCTTCTGGACGAGCTGCACTGCACGAGCAGC 970
Db 601 GCCTCAGGACCGCGGCTTCTCTCTTCTTCTGGACGAGCTGCACTGCACGAGCAGC 660
QY 971 ATCA 974
Db 661 ATCA 664

RESULT 11
LOCUS BG703589
DEFINITION 60268426F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4818775 5',
mRNA sequence.
ACCESSION BG703589
VERSION BG703589.1 GI:13976072
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0721 row: d column: 08
High quality sequence stop: 765.
FEATURES
Location/Qualifiers
1..851
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4818775"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
gtcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH MGC Library."

ORIGIN
Query Match 15.5%; Score 594; DB 12; Length 851;
Best Local Similarity 100.0%; Pred. No. 7e-103;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 GGTGAGCTGGCTCGAGCACTACTTCTGCGCGCGCTGCATCAGGAGCACTGGGTGG 725
Db 117 GGTGAGCTGGCTCGAGCACTACTTCTGCGCGCGCTGCATCAGGAGCACTGGGTGG 176
QY 726 GCAGAGCGGAGGCGCGCGGAGTCCCGAGTCCGCGCGCACTGCGGAGCCGCG 785
Db 177 GCAGAGCGGAGGCGCGCGGAGTCCCGAGTCCCGCGCGCACTGCGGAGCCGCG 236
QY 786 GCTGCGCGCCAGCTCAAGCTGGCCAACTGTCGAGGCGCTACAGCTCTTCCGCTGGA 845

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Db 237 GCTGGGGCCAGCCCTCAAGCTGGCCCAACATCTGTGGAGCGCTACAGCTCTTCCCGCTGA 296
QY 846 CCGCATCTCTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 905
Db 297 CGCCATCTCTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356
QY 906 CTTCTGCTCTACGGACCGCGCGCTTCTCTGCTTCTTCTGCGACGAGCTGCACTGCACGA 965
Db 357 CTTCTGCTCTACGGACCGCGCGCTTCTCTGCTTCTTCTGCGACGAGCTGCACTGCACGA 416
QY 966 GCAGCATCAGGTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1025
Db 417 GCAGCATCAGGTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 476
QY 1026 CCAACTTCAGGCGCCCTTCAAGACAGCAGCGCGGGAACACACCGGAGCGCTGCACTGCTCAA 1085
Db 477 CCAACTTCAGGCGCCCTTCAAGACAGCAGCGCGGGAACACACCGGAGCGCTGCACTGCTCAA 536
QY 1086 CGGCAACTGCGGAGACCAAGTCTTCCACCAAGAGCGCTGCGGACCACTATCGGCGAGGC 1145
Db 537 GCGCAACTGCGGAGACCAAGTCTTCCACCAAGAGCGCTGCGGACCACTATCGGCGAGGC 596
QY 1146 CTTGAGCGGCTGCACCGCGCTGCTGCTGAACGCGCAGAGCGCATGCTAGAGGAGCTGGA 1205
Db 597 CTTGAGCGGCTGCACCGCGCTGCTGCTGAACGCGCAGAGCGCATGCTAGAGGAGCTGGA 656
QY 1206 GCGGAGCACGCGCGCGCGCGCGCTGACCGCATCGAGCAGCAAAAGTCCAGCGCTACAG 1259
Db 657 GCGGAGCACGCGCGCGCGCGCGCTGACCGCATCGAGCAGCAAAAGTCCAGCGCTACAG 710

RESULT 12
LOCUS BU527114
DEFINITION AGENCOURT 10155963 NIH_MGC_101 Homo sapiens cDNA clone
IMAGE:6536868 5', mRNA sequence.
ACCESSION BU527114
VERSION BU527114.1 GI:22837555
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 931)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2698 row: o column: 12
High quality sequence stop: 552.
FEATURES
Location/Qualifiers
1..931
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6536868"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

```

from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes

FEATURES

source

Location/Qualifiers

1.682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-bid-j-07-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCGG. The tissue was provided by Dr. Gary W. Humminghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GGCCATGCGG

ORIGIN

Query Match 15.5%; Score 594; DB 13; Length 931;
Best Local Similarity 100.0%; Pred. No. 6.4e-103;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2118 CGACCGTGGCCACTGGAGACCTCAGCCAGTCTTTACCTCCAGCTCCAGCTCCAGCTCTGATAA 2177
Db 19 CGACCGTGGCCACTGGAGACCTCAGCCAGTCTTTACCTCCAGCTCCAGCTCCAGCTCTGATAA 78
QY 2178 ATGGAGTTCATTCCTTCTTCTTAACTCTCTTCAGCATCGATTTCTGTAGTCTG 2237
Db 79 ATGGAGTTCATTCCTTCTTCTTAACTCTCTTCAGCATCGATTTCTGTAGTCTG 138
QY 2238 ACCTTGATAGGGATACAGCTTTGATTCAGATGTGATGGCTTCTTCCTCAGGGCAACC 2297
Db 139 ACCTTGATAGGGATACAGCTTTGATTCAGATGTGATGGCTTCTTCCTCAGGGCAACC 198
QY 2298 CTGCCCCAACCTTCATCCCTCTTCTCAGGGCAGGGACTACCTTCCAGTGTCTCCCT 2357
Db 199 CTGCCCCAACCTTCATCCCTCTTCTCAGGGCAGGGACTACCTTCCAGTGTCTCCCT 258
QY 2358 CCAGCCAGCCCTGACCTCAGGAAGTGTACAGATGGCCAGTGTGGAGCCCGGAAG 2417
Db 259 CCAGCCAGCCCTGACCTCAGGAAGTGTACAGATGGCCAGTGTGGAGCCCGGAAG 318
QY 2418 ACACACAGCAGCTCTTATGTGCCATGCTTACCTTACCTTACCTTACCTTACCTTACCTT 2477
Db 319 ACACACAGCAGCTCTTATGTGCCATGCTTACCTTACCTTACCTTACCTTACCTTACCTT 378
QY 2478 GGCCATTTACCTTGACCCAGTCCACAGTGTGTACAGTAGTACCTTGTCTCTAGGGTTG 2537
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QY 2538 CTTGAGAGCAACCTCTCTGCTCCACCCACACCAAGAACTATATGTTCTTACTTCTCC 2597
Db 439 CTTGAGAGCAACCTCTCTGCTCCACCCACACCAAGAACTATATGTTCTTACTTCTCC 498
QY 2598 CACTGATCTGTGTGATGATGATGCTGTGCTGTGAGGACCTGTGTGTGATGATG 2657
Db 499 CACTGATCTGTGTGATGATGATGCTGTGCTGTGAGGACCTGTGTGTGATGATG 558
QY 2658 CACACATATAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2711
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RESULT 13
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LOCUS
DEFINITION
682 bp mRNA linear EST 01-NOV-2002
UI-H-FTI-bid-j-07-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone
UI-H-FTI-bid-j-07-0-UI 3', mRNA sequence.
CA309985
CA309985.1 GI:24473039
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail@nci.nih.gov
Tissue Procurement: Dr. Gary W. Humminghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained

ORIGIN

Query Match 15.3%; Score 587; DB 14; Length 682;
Best Local Similarity 100.0%; Pred. No. 1.8e-101;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3221 TGAGGCTTCCCTCTCCACCTTCACTCAGTTCCTCCAAATCTAAATTTTACAGGATTC 3280
Db 607 TGAGGCTTCCCTCTCCACCTTCACTCAGTTCCTCCAAATCTAAATTTTACAGGATTC 548
QY 3281 TGTGTTGGGGAACTTAAGTTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAATGTC 3340
Db 547 TGTGTTGGGGAACTTAAGTTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAATGTC 488
QY 3341 ATTTCCCTAGAGGAAGTTAGGCTGGTGAGCAAGCCCACTGCTGTTTCTGCGACA 3400
Db 487 ATTTCCCTAGAGGAAGTTAGGCTGGTGAGCAAGCCCACTGCTGTTTCTGCGACA 428
QY 3401 GCATCCCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGTTGCTGCCCC 3460
Db 427 GCATCCCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGTTGCTGCCCC 368
QY 3461 TTGGCTCTATCTCCCTGCCAGAGTGGGAATCGAGGAGTGGGCTGCAAGACTGAGCCTAA 3520
Db 367 TTGGCTCTATCTCCCTGCCAGAGTGGGAATCGAGGAGTGGGCTGCAAGACTGAGCCTAA 308
QY 3521 ATGCTCTCCCGGCTTGACTTTTCTTAGTCTCTGGGGCTTAGATTTGCACTTGGGGT 3580
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QY 3581 CTCTGACACAAACACACCATCCCAAGAGTCCGGAAGAGCTTAAACACAGGGGGTCTTAAA 3640
Db 247 CTCTGACACAAACACACCATCCCAAGAGTCCGGAAGAGCTTAAACACAGGGGGTCTTAAA 188
QY 3641 ATGCTCTCCCGGCTTGACTTTTCTTAGTCTCTGGGGCTTAGATTTGCACTTGGGGT 3700
Db 187 ATGCTCTCCCGGCTTGACTTTTCTTAGTCTCTGGGGCTTAGATTTGCACTTGGGGT 128
QY 3701 CCCTTCAACTACCAAGATCTGGGCGACCCAGCAGATATTTTATTTAAATGTTGCCCAT 3760
Db 127 CCCTTCAACTACCAAGATCTGGGCGACCCAGCAGATATTTTATTTAAATGTTGCCCAT 68

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QY 3761 TTTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGTCA 3807
DB |||||||||||||||||||||||||||||||||||||||||||||||||
67 TTTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGTCA 21

RESULT 14
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DEFINITION UI-H-DH0-aul-k-14-0-UI-s1 NCI CGAP_DH0 Homo sapiens cDNA clone
IMAGE:5871109 3', mRNA sequence.
ACCESSION BM994326
VERSION BM994326.1 GI:19719227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
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            /clone_lib="NCI CGAP DH0"
            /notes="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DH0 is a cDNA library containing the following
tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma
in Lung. The library was constructed according to Bonaldo,
Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pTT3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGATCATTCG.
TAG TISSUE=lung
TAG LIB=UI-H-DH0
TAG_SEQ=AGATCATTCG"

ORIGIN
Query Match 15.2%; Score 582; DB 12; Length 633;
Best Local Similarity 99.8%; Pred. No. 1.6e-100;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3192 CCACGGTCCGTCGACCAATAGATCTCTGAGGCGTCCCTCCCACTTCACCTAGT 3251
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633 CCACGGTCCGTCGACCAATAGATCTCTGAGGCGTCCCTCCCACTTCACCTAGT 574

QY 3252 TCCCAATCTAAATTTTACAGAGATCTGTGTTGGGGGAATTAAAGTCAGATCCAGAAC 3311
DB |||||||||||||||||||||||||||||||||||||||||||||||||
573 TCCCAATCTAAATTTTACAGAGATCTGTGTTGGGGGAATTAAAGTCAGATCCAGAAC 514

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QY 3312 CTTGGCTCAAGGGAGTCTGGGAAATGTCATTTCCCTAGAGGAAGTTAGGTTGGGTGA 3371
DB |||||||||||||||||||||||||||||||||||||||||||||||||
513 CTTGGCTCAAGGGAGTCTGGGAAATGTCATTTCCCTAGAGGAAGTTAGGTTGGGTGA 454

QY 3372 GCAGCCCCACCTCGGTTTTTCTGCGACAGCATCAATCGTGAAGAACTCGGGAGAGGGT 3431
DB |||||||||||||||||||||||||||||||||||||||||||||||||
453 GCAGCCCCACCTCGGTTTTTCTGCGACAGCATCAATCGTGAAGAACTCGGGAGAGGGT 394

QY 3432 GGAGTCCACATCTAGGTTGTCCTGCGCCCTTGGCTCTATCCCTGCCAGAGTGGAACT 3491
DB |||||||||||||||||||||||||||||||||||||||||||||||||
393 GGAGTCCACATCTAGGTTGTCCTGCGCCCTTGGCTCTATCCCTGCCAGAGTGGAACT 334

QY 3492 GGAGAGTGGCTGCAAGACTGAGCTAAATGTCTCCCGGCTTGTCTTTCTTTCTAG 3551
DB |||||||||||||||||||||||||||||||||||||||||||||||||
333 GGAGAGTGGCTGCAAGACTGAGCTAAATGTCTCCCGGCTTGTCTTTCTTTCTAG 274

QY 3552 TCCTGGGGCTTAGATTCGACCTTGGGGTCTCTGACACACACACCAATCCCAAGTAGCC 3611
DB |||||||||||||||||||||||||||||||||||||||||||||||||
273 TCCTGGGGCTTAGATTCGACCTTGGGGTCTCTGACACACACACCAATCCCAAGTAGCC 214

QY 3612 GGAAGAGCTAAACACAGGGGTTCTTAAATGCTGCTCCCGGCTTGTCTTTCTTTCTAG 3671
DB |||||||||||||||||||||||||||||||||||||||||||||||||
213 GGAAGAGCTAAACACAGGGGTTCTTAAATGCTGCTCCCGGCTTGTCTTTCTTTCTAG 154

QY 3672 GGCAAAAGGAATGTGACGCTTACCCCAACCTTCAACTACCAATCTGGGCCACCCCA 3731
DB |||||||||||||||||||||||||||||||||||||||||||||||||
153 GGCAAAAGGAATGTGACGCTTACCCCAACCTTCAACTACCAATCTGGGCCACCCCA 94

QY 3732 GCAGTATTTTATTAAATGTTGCCATTTTATGATGATCAATTTGTTAAAT 3791
DB |||||||||||||||||||||||||||||||||||||||||||||||||
93 GCAGTATTTTATTAAATGTTGCCATTTTATGATGATCAATTTGTTAAAT 34

QY 3792 AAAGTTACAGATGTCAAAAAAATAAAAAA 3824
DB |||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 15
LOCUS AU132503
DEFINITION AU132503 NT2RP3 Homo sapiens cDNA clone NT2RP3004617 5', mRNA
sequence.
ACCESSION AU132503
VERSION AU132503.1 GI:10992857
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 628)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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FEATURES
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Mon Aug 2 10:03:36 2004

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cells after 2-weeks retinoic acid (RA) induction"

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Query Match 13.9%; Score 533; DB 9; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.6e-91;
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 370 CCACCTACTTACGAGTCCCTCCGGGCTGGGCTCCACGGAGTCTCAGCGCGCACCCC 429
Db 1 CCACCTACTTACGAGTCCCTCCGGGCTGGGCTCCACGGAGTCTCAGCGCGCACCCC 60
QY 430 TTCTTCGGGTACCTCTCCGACAGACCCCTCCCTTCTCCGGTAGCTCCTACCCC 489
Db 61 TTCTTCGGGTACCTCTCCGACAGACCCCTCCCTTCTCCGGTAGCTCCTACCCC 120
QY 490 TGCTGTGGGGCTCGTCCCGCGCCAGCCCTCGGTGCTGCTCCGACAGCGCCGCGC 549
Db 121 TGCTGTGGGGCTCGTCCCGCGCCAGCCCTCGGTGCTGCTCCGACAGCGCCGCGC 180
QY 550 TCTCTAGCGCGCCCTCCCTCGGCGCCCTCTCTGCTGCGCCCTGCGCCATGCGC 609
Db 181 TCTCTAGCGCGCCCTCCCTCGGCGCCCTCTCTGCTGCGCCCTGCGCCATGCGC 240
QY 610 TGCAGCCTCAAGGACGAGTCTGTGCTCCATCTGCTGAGCATCTACAGGACCCGGTG 669
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QY 670 AGCCTGGGCTCGAGCACTTCTGCGCGCGCTGCAATCAGGAGCACTGGGTGGGCGAG 729
Db 301 AGCCTGGGCTCGAGCACTTCTGCGCGCGCTGCAATCAGGAGCACTGGGTGGGCGAG 360
QY 730 GAGGCGAGGGCGCGCGGAGTCCCGAGTCCCGGCGAGTTCGCGAGCGCGCGCTG 789
Db 361 GAGGCGAGGGCGCGCGGAGTCCCGGAGTCCCGGCGAGTTCGCGAGCGCGCGCTG 420
QY 790 GCGCCAGCCTCAAGTGGCCAAATCGTGGAGCGCTACAGTCTCCGCTGACGCC 849
Db 421 GCGCCAGCCTCAAGTGGCCAAATCGTGGAGCGCTACAGTCTCCGCTGACGCC 480
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Db 481 ATCCTCAAGCGCGCGCGCGGAGCCCTGCCAGGCGCGAGCAAGTCAA 533
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Job time : 9098 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Best Local Similarity 100.0%; Pred. No. 0;									
Matches 3826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	361	TTGAGTGCCTCACTACCTAGACTGCTCCCGGGCTGGCTCCAGCGGCTCTCAGGC	420						
QY	421	GGGACCCCTTCTCGGCTTACCTCTCCCGGACAGCACCCCTCTCTCTCTCTCTCTCTCT	480						
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QY	481	TCTACCCCTGCTGTCGGGCTCTGTCGGGCTCTGTCGGGCTCTGTCGGGCTCTGTCGG	540						
DB	481	TCTACCCCTGCTGTCGGGCTCTGTCGGGCTCTGTCGGGCTCTGTCGGGCTCTGTCGG	540						
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1381	CATGAGACCAACTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAG	1440
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1441	TACACCATCTGGAAGTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT	1500
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1921	ACCTTCCGCGAGAGTTCCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT	1980
1921	ACCTTCCGCGAGAGTTCCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT	1980
1981	GCCATGCGCAGAGAGTTCCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCT	2040

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2161	Db	AG	CTCCAG	CTCTAA	ATGG	AGTTCAT	TCCTT	ACTT	CTTAA	CTCTT	CCAG	CATC	2220													
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2281	Db	TT	CTCTC	TAGGG	CAAC	CCCTG	CCCA	CCCT	CA	TC	CCAT	TC	2340													
2341	Qy	CT	TTCCAG	TGTC	CTCC	TCCAG	CCCA	CCCT	GC	AGCT	CAG	GAAGTGT	CAG	ATGC	2400											
2341	Db	CT	TTCCAG	TGTC	CTCC	TCCAG	CCCA	CCCT	GC	AGCT	CAG	GAAGTGT	CAG	ATGC	2400											
2401	Qy	AG	TGGC	AGCC	CCGAA	AGAC	CAC	AG	CAC	CCCT	CTTAT	GTCC	ATG	CCGCT	TAAG	ACTTAC	CC	2460								
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2581	Qy	AT	GGTTC	CTACT	TTCC	CACTG	ATCTG	TG	GTG	GTG	GTG	ATG	ATG	TC	GTG	GTG	GTG	GTG	2640							
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2641	Qy	CAC	CTGT	GTAGT	TGAC	CA	CA	CTTAT	AGT	CA	TG	GC	CA	CC	CTT	CTG	CC	CA	AG	2700						
2641	Db	CAC	CTGT	GTAGT	TGAC	CA	CA	CTTAT	AGT	CA	TG	GC	CA	CC	CTT	CTG	CC	CA	AG	2700						
2701	Qy	GAG	GCA	AGG	TGAGG	GTATAC	CCAA	AG	CTCAT	GTG	CC	CA	CC	CTT	CTG	CC	CA	AG	2760							
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Db	3721	GGGCCACCCGACGATTTTTATTTAAATGTTGCCATTTTATGAGTTATGATCAATTT	3780
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Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
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Research Association for Biotechnology (JP)
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SQOLRVQEAQILQERLAETDRHTFLAGVASLERLKGKHETNLHPTDFPTSKYTG
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ORIGIN

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Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db      |||
Qy      |||

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Db      |||
Qy      |||

61  TTCTTCGGGTACCTTCCTCGGACAGCACCCCTCCCTTCCTCGGTAGTCTTACCCC 120
Db      |||
Qy      |||

490  TGCCTGTGGGGCTCGTCCCGCGCCAGCCCTCGGTGCTCCGACAGCGCGCGC 549
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Db      |||
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Db      |||
Qy      |||

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QY	2350	GTCTCCCTCCAGCCCGAGCCCTGACCTCAGGAAGTGTCAAGACATGGCCAGTAGTGGCAG	2409
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DB	2040	CCCGAAGACACACAGCACCCTCTTATGTGCCATGGCTTAGACTTACCCCTGACCAAGC	2099
QY	2470	TAGTGATGGGCCATTATACCTTTGACCCCACTGCTGTGTCTCAGAGTACTACTGGTCC	2529
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ACCESSION	BD156501		
VERSION	BD156501.1 GI:27862259		
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COMMENT	C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10, PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers (235). .(1659).		
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FT CDS (235). (1659).

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Db	61	TTCTCTCGGTTACCTCTCCGAGACAGCACCCCTCCCTTCTCCGGTAGCTCTACCCC	120
QY	490	TGCTCTGCGGCTGCTGCTCCCGGCGCCAGCCCTCGGTGCTCCGACAGCGCGCGC	549
Db	121	TGCTCTGCGGCTGCTGCTCCCGGCGCCAGCCCTCGGTGCTCCGACAGCGCGCGC	180
QY	550	TTCTCTAGCGCCCTCCGCTGCGGCGCCCTCTCTCTGCTGCTGCGCGCCATGGCG	609
Db	181	TTCTCTAGCGCCCTCCGCTGCGGCGCCCTCTCTCTGCTGCTGCGCGCCATGGCG	240
QY	610	TGCAAGCTCAAGGACGAGCTGCTGTGTCTCAATCTGCTGAGCATCTACAGGACCCGGTG	669
Db	241	TGCAAGCTCAAGGACGAGCTGCTGTGTCTCAATCTGCTGAGCATCTACAGGACCCGGTG	300
QY	670	AGCTTGGGCTCGAGGACTACTTCTGCGCGCGCTGCATCAGGAGCATCTGGGTGCGGCG	729
Db	301	AGCTTGGGCTCGAGGACTACTTCTGCGCGCGCTGCATCAGGAGCATCTGGGTGCGGCG	360
QY	730	GAGGCGAGGCGCGCGGCTGCGCGAGTGCAGGCGCGCGCTGCGCGAGCGCGCGCTG	789
Db	361	GAGGCGAGGCGCGCGGCTGCGCGAGTGCAGGCGCGCGCTGCGCGAGCGCGCGCTG	420
QY	790	GCGCCAGGCTCAAGTGGGCAACATCTGTGAGCGGCTACAGTCTCTTCCGCTGACGCC	849
Db	421	GCGCCAGGCTCAAGTGGGCAACATCTGTGAGCGGCTACAGTCTCTTCCGCTGACGCC	480
QY	850	ATTCCTCAAGCGCGCGCGGCTGCTGCTCTCTGCGAGCGCTGCACTGACGAGCTTTC	909
Db	481	ATTCCTCAAGCGCGCGCGGCTGCTGCTCTCTGCGAGCGCTGCACTGACGAGCTTTC	540
QY	910	TGCTCTCAGGACCGCGCGGCTGCTGCTCTCTGCGAGCGCTGCACTGACGAGCTTTC	969
Db	541	TGCTCTCAGGACCGCGCGGCTGCTGCTCTCTGCGAGCGCTGCACTGACGAGCTTTC	600
QY	970	CATCAGGTCACCGGATCAGACGCGCTTTCGAGAGCTGCAAGGAGGAGCTGAGGACCAA	1029
Db	601	CATCAGGTCACCGGATCAGACGCGCTTTCGAGAGCTGCAAGGAGGAGCTGAGGACCAA	660
QY	1030	CTTCAAGGCTTCAAGACAGCGGAGCACACCGAGCGCTGAGCTGCTCAAGCGA	1089
Db	661	CTTCAAGGCTTCAAGACAGCGGAGCACACCGAGCGCTGAGCTGCTCAAGCGA	720
QY	1090	CAACTGGGAGACCAAGTCTTCCACAGAGCTGCGGACCACTATCGGCGAGGCTTTC	1149
Db	721	CAACTGGGAGACCAAGTCTTCCACAGAGCTGCGGACCACTATCGGCGAGGCTTTC	780
QY	1150	GAGCGGCTGACCGGCTGCTGCTGAAACGCGAGAGGCTGCTGAGGAGCTGAGGCGG	1209
Db	781	GAGCGGCTGACCGGCTGCTGCTGAAACGCGAGAGGCTGCTGAGGAGCTGAGGCGG	840
QY	1210	GACAGCGCGGCTGACCGGCTGACCGAGTCCAGGCTGACGAGCTGACGAGCTG	1269
Db	841	GACAGCGCGGCTGACCGGCTGACCGAGTCCAGGAGTCCAGGCTGACGAGCTG	900
QY	1270	CGCAAGTTCAGGAGGAGCGGCTGCTGCTGAGAGCGGCTGCTGAGGAGCTGAGGCGG	1329
Db	901	CGCAAGTTCAGGAGGAGCGGCTGCTGCTGAGAGCGGCTGCTGAGGAGCTGAGGCGG	960
QY	1330	ACCTTCTGCTGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1389
Db	961	ACCTTCTGCTGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
QY	1390	AACCTCACATATGAGACTTCCCGACCTTCAAGTACACAGGCGCGCTGCTGCTGCTGCTG	1449

Db	1021	AACCTCACATATGAGACTTCCGACCTTCAAGTACACAGGCGCGCTGCTGCTGCTGCTG	1080
QY	1450	TGGAAGTCTCCTGTTCCAGGACATCCACCCAGTGCAGCGCGCTTAAACCTTGAGCCCGGC	1509
Db	1081	TGGAAGTCTCCTGTTCCAGGACATCCACCCAGTGCAGCGCGCTTAAACCTTGAGCCCGGC	1140
QY	1510	ACAGCCCAACAGCGCTGATTCCTGTCGAGCAGTGCACCATTTGGCTTACGGCAACTTG	1569
Db	1141	ACAGCCCAACAGCGCTGATTCCTGTCGAGCAGTGCACCATTTGGCTTACGGCAACTTG	1200
QY	1570	CACCCACAGCAGTGCAGGACTCGCAAGCGCTTCAATGTCAGGAGTGTGCTGCTGGGT	1629
Db	1201	CACCCACAGCAGTGCAGGACTCGCAAGCGCTTCAATGTCAGGAGTGTGCTGCTGGGT	1260
QY	1630	TCTGAAGCTTCACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1689
Db	1261	TCTGAAGCTTCACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1320
QY	1690	TGGTGATTCGGGCTGGCACACGAGCGCGCAAGCGCGCAAGCGCGCAAGCGCGCAAGCGCG	1749
Db	1321	TGGTGATTCGGGCTGGCACACGAGCGCGCAAGCGCGCAAGCGCGCAAGCGCGCAAGCGCG	1380
QY	1750	AGCCCGGCTTCTACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG	1809
Db	1381	AGCCCGGCTTCTACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG	1440
QY	1810	CCCTGGAGCGCGGCTTAAAGCTCCGGGCAAGCTTCAAGGTTGGGTGCTTCTTGGACTAT	1869
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QY	1870	GACCAAGCTTGTCTATCTTCTACAAATGCTGATGATGCTGATGCTGATGCTGATGCTGATG	1929
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Db	1621	AAGAACGTTTACGCGCTGCGGATCAACACCGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1680
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Db	1800	TCTGTAAAATGGAGGTTGCAATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1859
QY	2230	TAGCTCTGACCTTGTAGGATACAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2289
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QY	2350	GTCTCCCTCCAGCGCGCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG	2409
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QY	2410	CCGAAAGACACACAGCAGCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2469
Db	2040	CCGAAAGACACACAGCAGCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2099
QY	2470	TAGTGATGGGCAATTTACCTTGTACCCCTTGTACCCCTTGTACCCCTTGTACCCCTTGTACCCCTTGT	2529
Db	2100	TAGTGATGGGCAATTTACCTTGTACCCCTTGTACCCCTTGTACCCCTTGTACCCCTTGTACCCCTTGT	2159

QY	2530	TTAGGGTTGGCTCGAGAGCCAACTCTCTCTGCCACCCCCACACCAAGAACATATATGGTTTCCT	2589
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QY	2590	ACTTCTCCCACTGATCTGCTGTCTAGTGATGATGCTGTGTGGCCCTGTGGAAGGCACCTGGTA	2649
Db	2220	ACTTCTCCCACTGATCTGCTGTCTAGTGATGATGCTGTGTGGCCCTGTGGAAGGCACCTGGTA	2279
QY	2650	GTTGAGTCCACATATATAGTTCATGTGCGCCACCACTTCCTGCCCAAGCGGAGGACAG	2709
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Db	2700	CTGAATTTCCAGAACTCCAGCGCCAGATTCATCATCTGTTGTACACGAGGAAGCTG	2759
QY	3130	CCCCCATCTGCAGGAAGCCACTATGCCAGAAAGCTGCTGACTGCAGAACTAGGCTCCCTC	3189
Db	2760	CCCCCATCTGCAGGAAGCCACTATGCCAGAAAGCTGCTGACTGCAGAACTAGGCTCCCTC	2819
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Db	2820	TGCCACGCTCCGTGCCAGCCCAATAGATGCTCTGAGCGCTGCCCTCTCCCACTTCACTCA	2879
QY	3250	GTTCCTCCAAATCTAAATTTTATAAAGAGATTCCTGTTGGGGAACTTAAAGTCAGATCCAGA	3309
Db	2880	GTTCCTCCAAATCTAAATTTTATAAAGAGATTCCTGTTGGGGAACTTAAAGTCAGATCCAGA	2939
QY	3310	ACCTTGGCTGCAAGGGAGCTCTGGGAAATGCTATTCCTTAGAAGGAAGTTAGGGTGGGTG	3369
Db	2940	ACCTTGGCTGCAAGGGAGCTCTGGGAAATGCTATTCCTTAGAAGGAAGTTAGGGTGGGTG	2999
QY	3370	GAGCAAGCCCAACCTCGCTGTTTTCTGCCACAGCATCCCAATCTGTAGAGACTCGGAGAGG	3429
Db	3000	GAGCAAGCCCAACCTCGCTGTTTTCTGCCACAGCATCCCAATCTGTAGAGACTCGGAGAGG	3059
QY	3430	GTGAGATCCACATCTAGGGTTGTCTGCCCTTGGCTCTATCCCTGCCAGAGGTGGGAA	3489
Db	3060	GTGAGATCCACATCTAGGGTTGTCTGCCCTTGGCTCTATCCCTGCCAGAGGTGGGAA	3119
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QY	3550	AGTCTCTGGGGCTAGATTCTGCACTTGGGGTCTCTGACACACACACCATCCCAAGTAG	3609
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Qy	3610	CCGGAAGAGCTAAACACAGGGGGTTCTTTAAATGCTGCCCGCCACCCGGGGCTCCCT	3669
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Qy	3670	TGGGCAAAAGGAATGTGTCAGCCCTACCCCAACCCCTTCAACTACCAATCTGGGCCACCC	3729
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Qy	3730	CAGCAGTATTTTATTTAAATGTTGCCATTTTATGAGTTATGATCAATTTGTAATAA	3789
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RESULT 4			
AK001621			
LOCUS			
DEFINITION	AK001621	3436 bp mRNA linear	PRI 01-AUG-2002
ACCESSION		Homo sapiens CDNA FLJ10759 fis, clone NT2RP3004617, weakly similar	
VERSION	AK001621.1	GI:7022986	
KEYWORDS		oligo capping; fis (full insert sequence).	
SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		Isogai, T., Ota, T., Hayaishi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,	
		Nishikawa, T., Nagai, K., Sugeno, S., Ishibashi, T., Fujimori, K.,	
		Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Ishii, S., Kawai, Y.,	
		Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahashi, K.,	
		Masuho, Y. and Kanehori, K.	
TITLE		NED0 human cDNA sequencing project	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 3436)	
AUTHORS		Isogai, T. and Otsuki, T.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,	
		Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan	
		(E-mail:genomics@shri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	
COMMENT		NED0 human cDNA sequencing project supported by Ministry of	
		International Trade and Industry of Japan; cDNA full insert	
		sequencing; Research Association for Biotechnology; cDNA library	
		construction; 5'- & 3'-end one pass sequencing and clone selection;	
		Helix Research Institute (supported by Japan Key Technology Center	
		etc.) and Department of Virology, Institute of Medical Science,	
		University of Tokyo.	
FEATURES		Location/Qualifiers	
source		1..3436	
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		/cell_line="NT2"	
		/cell_type="teratocarcinoma"	
		/clone_lib="NT2rp3"	
		/note="Cloning vector: pME18SFL3-mRNA from NT2 neuronal	
		precursor cells after 2-weeks retinoic acid (RA)	

CDS

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
4. <i>Other</i>	
5. <i>Other</i>	
6. <i>Other</i>	
7. <i>Other</i>	
8. <i>Other</i>	
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ORIGIN		Query Match		Score 3420.2;		DB 9;		Length 3436;	
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DB	1	CCACTACCTTAGACTGCCCTCCGGGCTGGCGTCCCAAGAGTCTCAGCGCGCACCCC	60						
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DB	61	TTCTCTCGCGTTACCTCTTCGGAGACACCCCTCTCTTCCGGTAGCTCTACCCC	120						
QY	490	TGCTGTGCGGGCTCGTCCCGCGCCAGCCCTCGGTGCTGCTCCGACAGCGCGCGC	549						
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QY	550	TCTCTAGCGCCCGCCCTGCGCCCTCGGCGCCCTCTCTGCTGCGCCCTGGCGCCATGGC	609						
DB	181	TCTCTAGCGCCCGCCCTGCGCCCTCGGCGCCCTCTCTGCTGCGCCCTGGCGCCATGGC	240						
QY	610	TGCGAGCTCAAGGACGAGCTGTGTCTCCATCTGCTGAGCATCTACAGGACCCGGTG	669						
DB	241	TGCGAGCTCAAGGACGAGCTGTGTCTCCATCTGCTGAGCATCTACAGGACCCGGTG	300						
QY	670	AGCTTGGGCTGAGGACATCTTCTGCGCGCGCTGCATCAGGAGCATGGGTGGCGAG	729						
DB	301	AGCTTGGGCTGAGGACATCTTCTGCGCGCGCTGCATCAGGAGCATGGGTGGCGAG	360						
QY	730	GAGGCGAGGGCGCGGAGCTGCGCGAGTCCCGCGCACCTTTCGCGAGCCCGCGTG	789						
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QY	970	CATCAGGTCAACGGGCTGAGGAGCGGCTTTCGAGAGTGGAGGAGTGAAGGACCA	1029						
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DB	661	CTTCAGGCGCTTCAAGGAGCGGAGCACACGAGCGCTGCGAGTGGCTCAAGCGA	720						
QY	1090	CAACTGCGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCACTATCGGAGGCGCTTC	1149						
DB	721	CAACTGCGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCACTATCGGAGGCGCTTC	780						
QY	1150	GAGCGGTGACCGGCTGCTGCTGAAAGCGGAGGCGATCTAGAGGAGCTGAGGCG	1209						
DB	781	GAGCGGTGACCGGCTGCTGCTGAAAGCGGAGGCGATCTAGAGGAGCTGAGGCG	840						
QY	1210	GACACGGCGCGACGCTGACGAGCATCGAGCAGAAAGTCCAGCGCTACAGCAGAGCTG	1269						
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QY	1270	GCGAGGTCCAGGAGGAGCGGACGATCTCTGAGGAGCGGCTGGCTGAAACCGACCGGAC	1329						
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DB	961	ACCTTCTCGGCTGGGGTGGCCCTCACTGTCCGAGCGCTCAAGGAAAAATCATGAGACC	1020						
QY	1390	AACCTCACATATGAAGACTTCCCGACTCCAGTACACAGGCCCCCTGAGTACACATC	1449						
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DB	1980	GTCTCCCTCCAGCCCGCTGACCTCAGGAGGTGTGACGATGGCGAGTAGTGGCAG	2039						
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Db	2040	CCCGAAAGACACACAGCACCCCTCTATATGTGCCATAGCCTTAAGCTTACCCCTGACCAAGC	2099
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Db	2400	GCCTCCCTGGATGATCAGAGTCCCCAGTAGCTCTGAACAAGAGTCCAGCCACCTCTTC	2459
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ACCESSION	BC001222		
VERSION	BC001222.1	GI:12654758	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Workley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Rodrigues, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26)	16899-16903 (2002)
PUBMED	22388257		
REFERENCE	2	(bases 1 to 3259)	
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		

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 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalrus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Teal, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAL Plate: 6 Row: J Column: 17
 This clone was selected for full length sequencing because it
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RESULT 6
BC007999
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

BC007999 3259 bp mRNA linear PRI 03-OCT-2003
Homo sapiens hypothetical protein FLJ10759, mRNA (cDNA clone
MGC:15757 IMAGE:3357436), complete cds.
BC007999
BC007999.1 GI:14124949
MGC.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3259) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T.J., Max,S.I., Wang,J., Heide,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.C., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schwartz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257 12477932 2 (bases 1 to 3259)
REFERENCE	Strausberg,R. Direct Submission Submitted (15-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remain@nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ruben Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
REMARK	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 23 Row: a Column: 20. Location/Qualifiers 1. .3259 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:15757 IMAGE:3357436" /tissue_type="Eye, retinoblastoma" /clone_lib="NIH_MGC_16" /lab_host="DH10B-R" /note="Vector: pOTB7" 1. .3259 /gene="FLJ10759" /db_xref="LocusID:55223" 34..1461 /codon_start=1 /product="hypothetical protein FLJ10759" /protein_id="AAH07999.1"
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gene	
CDS	

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REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Dec 19, 2003 this sequence version replaced gi:15079757.
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ARCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@hgrl.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it
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identity to protein.

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RESULT 7
BC011689
LOCUS
DEFINITION
MGC:19672 IMAGE:3353034, complete cds.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carrin, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Jones, S.J., and Marra, M.A.

Schmerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)

2 (bases 1 to 3259)
Strausberg, R.
Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

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RESULT 12

AC022262/c

LOCUS

DEFINITION

AC022262

AC022262

HTG; HTGS PHASE1; HTGS_DRAFT.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC022262 164950 bp DNA linear HTG 07-JUL-2000
Homo sapiens chromosome 1 clone RP11-150F21, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
AC022262
AC022262.4 GI:8569825
HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 164950)
Waterston,R.H.
Direct Submission
Submitted (27-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7321934.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0150F21
----- Summary Statistics -----
Sequencing vector: M13; 75%
Chemistry: Dye-primer ET; 75% of reads
Assembly: Dye-terminator Big Dye; 25% of reads
Consensus quality: 163188 bases at least Q40
Consensus quality: 163696 bases at least Q30
Consensus quality: 163935 bases at least Q20
Insert size: 172000; agarose-fp
Insert size: 164650; sum-of-contigs
Quality coverage: 7.83 in Q20 bases; agarose-fp
Quality coverage: 8.20 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1 8662: contig of 8662 bp in length
* 8663 8762: gap of unknown length
* 8763 27020: contig of 18258 bp in length
* 27021 27120: gap of unknown length
* 27121 78035: contig of 50915 bp in length
* 78036 78135: gap of unknown length
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FEATURES

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RESULT 13
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LOCUS
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ACCESSION AL662907
VERSION AC026053
KEYWORDS
SOURCE HTG.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 64693)
Van Hellmond, Z.
Direct Submission
Submitted (18-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:20145349.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
Rpl1-131M11 is from the library RPl1-11.1 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
Draft Sequence Produced by Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
http://genome.wustl.edu/gsc/index.shtml.

FEATURES
source

Location/Qualifiers
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ORIGIN

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Matches 2349; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
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Db	6563	ACTGCAAGCTAGGCTCCCTGTGCGAGGTCGGTCCAGCAATAGATGTCTTGGAGCT	6504	TITLE			
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 VERSION HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
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 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 136095)
 Wen, G., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N.,
 Lehmann, R., Menzel, U., Polley, A., Reichwald, K., Schudy, A.,
 Siddiqui, R., Taudien, S., Schilabel, M.B., Schlegelberger, B.,
 Siebert, R., Rosenthal, A. and Platzter, M.
 Chromosome 8 genomic sequence
 Unpublished

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Polley, A., Nordiek, G., Schlegelberger, B., Drescher, B., Weber, J.,
 Schatttey, R. and Rosenthal, A.
 Direct Submission
 Submitted (21-JUN-1999) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
 On Oct 24, 2001 this sequence version replaced gi:14277237.
 ----- Genome Center
 Center: Institute of Molecular Biotechnology
 Center code: IMB
 Web site: <http://genome.imb-jena.de/>
 Contact: gsj-submit@genome.imb-jena.de
 ----- Project Information
 Center project name: H176
 Center clone name: CTA-392H5
 ----- Summary Statistics
 Sequencing vector: M13; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 122353 bases at least Q40
 Consensus quality: 127794 bases at least Q30
 Consensus quality: 131293 bases at least Q20
 Quality coverage: 5.82 x in Q20 bases; sum-of-contigs

Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality 10.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 1803 1902: gap of unknown length
 * 1903 5293: contig of 3391 bp in length

5294 5393: gap of unknown length
 5394 9774: contig of 4581 bp in length
 9775 10074: gap of unknown length
 10075 15065: contig of 4991 bp in length
 15066 15165: gap of unknown length
 15166 20118: contig of 4953 bp in length
 20119 20218: gap of unknown length
 20219 26289: contig of 6071 bp in length
 26290 26389: gap of unknown length
 26390 35964: contig of 9575 bp in length
 35965 36064: gap of unknown length
 36065 46363: contig of 10299 bp in length
 46364 46463: gap of unknown length
 46464 58765: contig of 12302 bp in length
 58766 58865: gap of unknown length
 58866 77219: contig of 18354 bp in length
 77220 77319: gap of unknown length
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CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the expression of
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1, and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence is the cDNA encoding CAR-1
XX
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QY 1441 TACACATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCAGCGCGCTTAACCTTG 1500
DB 1441 TACACATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCAGCGCGCTTAACCTTG 1500
QY 1501 GACCGGCGACAGCGCGCGCGCTGATCTCTGCGAGCGCTGACCAATGTTGGCTTAC 1560

Db 1501 GACCCGGGACAGCCACCAGCGCTGATCCTGTGTGGAGCACTGCACCAATTGTGGCTTAC 1560
QY 1561 GGCAACTTGCACCCACAGCCACTGCGAGGACTCCGAAAGCGCTTCGATGTGGAGGTGTG 1620
Db 1561 GGCAACTTGCACCCACAGCCACTGCGAGGACTCCGAAAGCGCTTCGATGTGGAGGTGTG 1620
QY 1621 GTCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTGCGAGGTGGTGGCGGAG 1680
Db 1621 GTCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTGCGAGGTGGTGGCGGAG 1680
QY 1681 AAGACCCAGTGGGTGATCGGGCTTGGCACACGAAGCCGCAAGCCGCAAGGCGCAGATCCAG 1740
Db 1681 AAGACCCAGTGGGTGATCGGGCTTGGCACACGAAGCCGCAAGGCGCAGATCCAG 1740
QY 1741 ATCCAGCCAGCGCGGCTTCTACTGATCGTGTGATGCAAGCCGCAAGGCGCAGATCCAG 1800
Db 1741 ATCCAGCCAGCGCGGCTTCTACTGATCGTGTGATGCAAGCCGCAAGGCGCAGATCCAG 1800
QY 1801 TGCACGGAGCCCTGGACGGGCTTAAAGCTCCGGGACAAGCTTCACAAGGTGGGTGCTTC 1860
Db 1801 TGCACGGAGCCCTGGACGGGCTTAAAGCTCCGGGACAAGCTTCACAAGGTGGGTGCTTC 1860
QY 1861 CTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGATGACATGCTCGCTCTAC 1920
Db 1861 CTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGATGACATGCTCGCTCTAC 1920
QY 1921 ACCTTCGGGAGAGTTCCTTGGCAAGCTTGCTCTTACTTACAGCCGTGGCCAGAGCCAC 1980
Db 1921 ACCTTCGGGAGAGTTCCTTGGCAAGCTTGCTCTTACTTACAGCCGTGGCCAGAGCCAC 1980
QY 1981 GCGAATGGCAAGAACCTTCAGCGGCTGGGATCAACACCGTCCGATCTAGTCCAGGCGAG 2040
Db 1981 GCGAATGGCAAGAACCTTCAGCGGCTGGGATCAACACCGTCCGATCTAGTCCAGGCGAG 2040
QY 2041 AAGGAGACCAACCTCTCTGGGACCACTGCCACTGCAAGAGCCCTGCCAGGAATAG 2100
Db 2041 AAGGAGACCAACCTCTCTGGGACCACTGCCACTGCAAGAGCCCTGCCAGGAATAG 2100
QY 2101 AAGACTGACTCCAGCCACCGTGGCCACTGAGACCTCAGGCGAGTGTTCACCTCC 2160
Db 2101 AAGACTGACTCCAGCCACCGTGGCCACTGAGACCTCAGGCGAGTGTTCACCTCC 2160
QY 2161 AGCCTCCAGTCTGTAAATGGAGTTGCAATCCCTACTTCTTAAACTCTCTTCCAGCATC 2220
Db 2161 AGCCTCCAGTCTGTAAATGGAGTTGCAATCCCTACTTCTTAAACTCTCTTCCAGCATC 2220
QY 2221 GATGTTCTGTAGTCTGTGATAGGAGTACAGCTTTGATCCAAAGGATGTGACATGGC 2280
Db 2221 GATGTTCTGTAGTCTGTGATAGGAGTACAGCTTTGATCCAAAGGATGTGACATGGC 2280
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Db 2281 TTCTCTCAGGGCAACCCCTGCGCCACCTCATCCCACTTCTCAGGGCGAGGACTA 2340
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Db 3001 GACAAGATTTACTACTCTGGCCCTGGTGGCTTGCAGAAATTTGTTGGAAGAGCTGGAGAAG 3060
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Db 3061 CAGACTCTCTGAATTTCCAGGAATCCAGAGGCCAGATTCATCATGTCTGTGTGACCA 3120
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Db 3121 GGAAAGCTCCCCCACTCTGCAGGAAGCCACTATGCGAGAAAGCTGTGACTGCAGAACTA 3180
QY 3181 GGTCTCCTCTGCCACCGTCCGTCCGAGCAATAGATGTCTGAGGCTGCGCCCTCTCCCA 3240
Db 3181 GGTCTCCTCTGCCACCGTCCGTCCGAGCAATAGATGTCTGAGGCTGCGCCCTCTCCCA 3240
QY 3241 CTTCTACTGAGTTCCCAAAATCTAAATTTTACAGAGATCTGTGTTGGGGAATCTTAAGTC 3300
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Db 3301 AGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAATGTCAITTTCCCTAGAGAAAGTTA 3360
QY 3361 GGTGGGTGGAGCAAGCCCACTGCGTTTTCGCCACAGCATCCAACTGTTGAAGAACT 3420
Db 3361 GGTGGGTGGAGCAAGCCCACTGCGTTTTCGCCACAGCATCCAACTGTTGAAGAACT 3420
QY 3421 CGGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCGCCCTTGGCTCTATCCCTGCCAG 3480
Db 3421 CGGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCGCCCTTGGCTCTATCCCTGCCAG 3480
QY 3481 AGGTGGAACTGGAGAGTGGCTGCAAGACTGAGCCTAAATGTCTCCCGGCTTGTACT 3540
Db 3481 AGGTGGAACTGGAGAGTGGCTGCAAGACTGAGCCTAAATGTCTCCCGGCTTGTACT 3540
QY 3541 TTCTCTTCTAGTCTGGGCTTAGATCTGCACTTGGGTCTCTGACACACACCATC 3600
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QY 3601 CCAGATAGCCGGAAGACTAAACAAGGGGTTCTTAAATGGCTGCCCGCCACCGC 3660
Db 3601 CCAGATAGCCGGAAGACTAAACAAGGGGTTCTTAAATGGCTGCCCGCCACCGC 3660
QY 3661 GGCCTCCCTTGGGCAAAAAGGAATGTGAGCCCTACCCCAACCTTCAATACAGAATCT 3720
Db 3661 GGCCTCCCTTGGGCAAAAAGGAATGTGAGCCCTACCCCAACCTTCAATACAGAATCT 3720

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QY 3721 GGCCACCCGAGCAGTATTTTATTTAAATGTTGCCATTTTATGAGTTATGATCAATT 3780
Db 3721 GGCCACCCGAGCAGTATTTTATTTAAATGTTGCCATTTTATGAGTTATGATCAATT 3780
QY 3781 TGTATTAAATTTAAAGTTACAGATGTCACAAAAAATAAAAAA 3826
Db 3781 TGTATTAAATTTAAAGTTACAGATGTCACAAAAAATAAAAAA 3826

RESULT 2
AAH14509
ID AAH14509 standard; cDNA; 3436 BP.
XX AAH14509;
XX AC
XX XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:12036.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 12036; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX length cDNAs defined in the specification. Where a primer set comprises:
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX complementary strand of a polynucleotide which comprises one of the 5602
XX nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 3'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in the
XX specification. The primer sets can be used in antisense therapy and in
XX gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
XX represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX oligonucleotides, all of which are used in the exemplification of the
XX present invention
XX
XX Sequence 3436 BP; 731 A; 1126 C; 901 G; 678 T; 0 U; 0 Other;
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Query Match 89.4%; Score 3420.2; DB 4; Length 3436;
Best Local Similarity 99.94; Pred. No. 0;
Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 370 CCACTACCTCTAGACTGCCCTCCGGGCTGGCGTCCACGAGAGTCTCAGCGGGCACC 429
Db 1 CCACTACCTCTAGACTGCCCTCCGGGCTGGCGTCCACGAGAGTCTCAGCGGGCACC 60

QY 430 TTCTTGGCGTTACCTCTTCCGAGACAGACCCCTCCCTTCTCCGGTAGTCTTACCCC 489
Db 61 TTCTTGGCGTTACCTCTTCCGAGACAGACCCCTCCCTTCTCCGGTAGTCTTACCCC 120

QY 490 TGCTGTGGGGCTCTGTCGCCCGCCAGCCCTCGGTGCTCGCTCCGACAGGCCCGCGC 549
Db 121 TGCTGTGGGGCTCTGTCGCCCGCCAGCCCTCGGTGCTCGCTCCGACAGGCCCGCGC 180

QY 550 TCTCTCAGCGCCGCCCTTGGCCCTCGGGCCCTCTCTGTGCTGCTGCGGCCCATGGCG 609
Db 181 TCTCTCAGCGCCGCCCTTGGCCCTCGGGCCCTCTCTGTGCTGCTGCGGCCCATGGCG 240

QY 610 TGCAGCCTCAAGAGCAGAGTCTGTGCTTCCATCTGCTGAGCATCTACCAGACCCGGTG 669
Db 241 TGCAGCCTCAAGAGCAGAGTCTGTGCTTCCATCTGCTGAGCATCTACCAGACCCGGTG 300

QY 670 AGCTGGGCTGCGAGCAGTCTTCTGCGCGCTGTCATCAGGAGCATCTGGGTGGCGAG 729
Db 301 AGCTGGGCTGCGAGCAGTCTTCTGCGCGCTGTCATCAGGAGCATCTGGGTGGCGAG 360

QY 730 GAGCGCAGGGCGCCCGCGACTGCCCCAGTGGCGGCGACGTTTCGCGGACCCCGCGTG 789
Db 361 GAGCGCAGGGCGCCCGCGACTGCCCCAGTGGCGGCGACGTTTCGCGGACCCCGCGTG 420

QY 790 GCGCCAGCCTCAAGCTGGGCCAATCGTGGAGCGCTACAGCTCTTCCGCTGGAGCGCC 849
Db 421 GCGCCAGCCTCAAGCTGGGCCAATCGTGGAGCGCTACAGCTCTTCCGCTGGAGCGCC 480

QY 850 ATCTCAAGCGCGCCCGCGCGCCCTGCGCAGCGCACGACAAAGTCAAGTCTTTC 909
Db 481 ATCTCAAGCGCGCCCGCGCGCCCTGCGCAGCGCACGACAAAGTCAAGTCTTTC 540

QY 910 TGCCTCAGGACCGCGCGCTTCTCTGTTTTCGACGAGCGCTGCACTGCAGAGAG 969
Db 541 TGCCTCAGGACCGCGCGCTTCTCTGTTTTCGACGAGCGCTGCACTGCAGAGAG 600

QY 970 CATCAGTCAACCGCATCGACGACGCTTCCAGCAGCTGACAGAGGAGCTGAAGACCAA 1029
Db 601 CATCAGTCAACCGCATCGACGACGCTTCCAGCAGCTGACAGAGGAGCTGAAGACCAA 660

QY 1030 CTTTCAGGCGCTTCAAGACAGCGAGCGGGAACACACCGAAGCGCTGCAGTCTCTCAAGCGA 1089
Db 661 CTTTCAGGCGCTTCAAGACAGCGAGCGGGAACACACCGAAGCGCTGCAGTCTCTCAAGCGA 720

QY 1090 CAACTGGCGGAGACCAAGTCTTCCACCAAGAGCTGGGACCACTATCGGGAGGCTTTC 1149
Db 721 CAACTGGCGGAGACCAAGTCTTCCACCAAGAGCTGGGACCACTATCGGGAGGCTTTC 780

QY 1150 GAGCGGCTGCACCGCTGCTGCGTGAACGCGAGAGGCTATGAGAGAGCTGAGGCG 1209
Db 781 GAGCGGCTGCACCGCTGCTGCGTGAACGCGAGAGGCTATGAGAGAGCTGAGGCG 840

QY 1210 GACACGGCCCGCAGCTGACCGCATCGACAGAGAAAGTCCAGCGCTACAGCCAGAGCTG 1269
Db 841 GACACGGCCCGCAGCTGACCGCATCGACAGAGAAAGTCCAGCGCTACAGCCAGAGCTG 900

QY 1270 CGCAAGTCTCAGGAGGAGGCCAGATCTGACGAGCGGCTGGCTGAACCGACCGGCAC 1329
Db 901 CGCAAGTCTCAGGAGGAGGCCAGATCTGACGAGCGGCTGGCTGAACCGACCGGCAC 960

QY 1330 ACCTTCTGCTGGGTGGGTGGCTCTCATGTCGCGAGCGGCTCAAGGGGAAAAATCCATGAGCC 1389
Db 961 ACCTTCTGCTGGGTGGGTGGCTCTCATGTCGCGAGCGGCTCAAGGGGAAAAATCCATGAGCC 1020
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QY	1651	GTCCACTACTGGAGGTGGTGGCGGGAAGACCCAGTGGGTGATCGGGCTGGGCACAC	1710
Db	1090	GTCCACTACTGGAGGTGGTGGCGGGAAGACCCAGTGGGTGATCGGGCTGGGCACAC	1149
QY	1711	GAAGCCGCAAGCCGCAAGGCGAGCATCCAGTCCAGCCAGCCGCGCTTCTACTGCATC	1770
Db	1150	GAAGCCGCAAGCCGCAAGGCGAGCATCCAGTCCAGCCAGCCGCGCTTCTACTGCATC	1209
QY	1771	GTGATGCAAGTGGCAACGAGTACAGGCGCTGCAAGGAGCCCTGGAGCGCGCTTAAAGTC	1830
Db	1210	GTGATGCAAGTGGCAACGAGTACAGGCGCTGCAAGGAGCCCTGGAGCGCGCTTAAAGTC	1869
QY	1831	CGGGAAGCTTACAAAGGTGGGTGCTTCCCTGAGCTATGACCAAGGCTGCTCATCTTC	1890
Db	1270	CGGGAAGCTTACAAAGGTGGGTGCTTCCCTGAGCTATGACCAAGGCTGCTCATCTTC	1329
QY	1891	TACAATGCTGATGACATGCTCGCTCTACACCTTCCGCGAGAGTTTCCCTGGCAAGCTC	1950
Db	1330	TACAATGCTGATGACATGCTCGCTCTACACCTTCCGCGAGAGTTTCCCTGGCAAGCTC	1389
QY	1951	TGCTCTTACTTACGCTCGGCGAGGCGACGCAATGGCAAGAACGTTACGCGCTGCGG	2010
Db	1390	TGCTCTTACTTACGCTCGGCGAGGCGACGCAATGGCAAGAACGTTACGCGCTGCGG	1449
QY	2011	ATCAACACCGTCCGCAATCTAGTCCAGGCAAGAGGACACACACTTCTGGGACACTGC	2070
Db	1450	ATCAACACCGTCCGCAATCTAGTCCAGGCAAGAGGACACACACTTCTGGGACACTGC	1509
QY	2071	CACCTCAAGAGCCCTGCCAGGAAGATAGAACCTTGGACTCCAGCCACCGTGGCCAC	2130
Db	1510	CACCTCAAGAGCCCTGCCAGGAGATAGAACCTTGGACTCCAGCCACCGTGGCCAC	1568
QY	2131	TGGAGACCTCAGCCAGTTGTTTACCTCCAGCTCCAGCTCTGTAATAATGGAGTTGCAT	2190
Db	1569	TGGAGACCTCAGCCAGTTGTTTACCTCCAGCTCCAGCTCTGTAATAATGGAGTTGCAT	1628
QY	2191	TCCTTACTTCTTAACTCTTCCAGCATCGATGTTCTGATGCTGACCTTGATAGGGA	2250
Db	1629	TCCTTACTTCTTAACTCTTCCAGCATCGATGTTCTGATGCTGACCTTGATAGGGA	1688
QY	2251	TACAGCTTTGATCCAAAGGATGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCTT	2310
Db	1689	TACAGCTTTGATCCAAAGGATGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCTT	1748
QY	2311	GATCCCATCTTCTCAGGGGAGGGAGCTACCTTCCAGTGTCTCCCTCAGCCAGCCCT	2370
Db	1749	GATCCCATCTTCTCAGGGGAGGGAGCTACCTTCCAGTGTCTCCCTCAGCCAGCCCT	1808
QY	2371	GACCTCAGGAAGTGTGAGAGCATGGCCAGTGTGGCAGCCGGAAGACACACAGCACCC	2430
Db	1809	GACCTCAGGAAGTGTGAGAGCATGGCCAGTGTGGCAGCCGGAAGACACACAGCA-CC	1867
QY	2431	TCTTATGTCCTAAGCTTAAAGCTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCTT	2490
Db	1868	TCTTATGTCCTAAGCTTAAAGCTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCTT	1927
QY	2491	TGACCCAGTCCACAGTGTGACAGTAGTACTGTCTAGGTGCTTCTGAGGCGCAAC	2550
Db	1928	TGACCCAGTCCACAGTGTGACAGTAGTACTGTCTAGGTGCTTCTGAGGCGCAAC	1987
QY	2551	CTCTCTGCGCACCCCCACACCAAGAACTATATGGTTCTTCTCTCCACTGATCTGCTG	2610
Db	1988	CTCTCTGCGCACCCCCACACCAAGAACTATATGGTTCTTCTCTCCACTGATCTGCTG	2047
QY	2611	GTCAAGTATGATGCTGTGGCTGTGGAGGCACTTGGTAGTTGAGTCCACATATAGT	2670
Db	2048	GTCAAGTATGATGCTGTGGCTGTGGAGGCACTTGGTAGTTGAGTCCACATATAGT	2107
QY	2671	CATGTGCCACCACTTCTGCGCCACAGGCGGAGGAGCAGGGTGAGGGTATACCCAAAGCT	2730
Db	2108	CATGTGCCACCACTTCTGCGCCACAGGCGGAGGAGCAGGGTGAGGGTATACCCAAAGCT	2167

QY	2731	GATGCAGAGCCCATTTAGCCTTAAAGCAACTGCGAGGACAAGCCTCCTTGGATGATCGAGGT	2790
Db	2168	GATGCAGAGCCCATTTAGCCTTAAAGCAACTGCGAGGACAAGCCTCCTTGGATGATCGAGGT	2227
QY	2791	CCCCAGTAGCTCTGAACAAGAGTCCAGCCAAACCTCTTTCAGCCAGGCTCTGTGACCTGC	2850
Db	2228	CCCCAGTAGCTCTGAACAAGAGTCCAGCCAAACCTCTTTCAGCCAGGCTCTGTGACCTGC	2287
QY	2851	TAGGTCGAGGAGCTTCCAGAAAGCAGTTGTTGTAATTAGGACCCCAAGCACTGGAGGGG	2910
Db	2288	TAGGTCGAGGAGCTTCCAGAAAGCAGTTGTTGTAATTAGGACCCCAAGCACTGGAGGGG	2347
QY	2911	CTGTCGGCTAGACCCCTTGTTCAGACTTGGCATCTATCTCAGTTAGGATCTCTGCTGAGAA	2970
Db	2348	CTGTCGGCTAGACCCCTTGTTCAGACTTGGCATCTATCTCAGTTAGGATCTCTGCTGAGAA	2407
QY	2971	AACAAGAGCCACTTGTAGCTGGTTTAAATTAGACAAGGATTTACTACTGCGCCCTCGTGG	3030
Db	2408	AACAAGAGCCACTTGTAGCTGGTTTAAATTAGACAAGGATTTACTACTGCGCCCTCGTGG	2467
QY	3031	CTTGTAAAATTTGTGAAGAGCTGGAGAACAGACTCTCTGTAATTTCCAGGAACTCCCA	3090
Db	2468	CTTGTAAAATTTGTGAAGAGCTGGAGAACAGACTCTCTGTAATTTCCAGGAACTCCCA	2527
QY	3091	GGCCAGATTCATCATGTCTGTGTGACCAAGAAAGCTGCCCCCATCTCGAGAAAGCCAC	3150
Db	2528	GGCCAGATTCATCATGTCTGTGTGACCAAGAAAGCTGCCCCCATCTCGAGAAAGCCAC	2587
QY	3151	TATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCTCTGCGCACGGTCCGTGCCAGCCA	3210
Db	2588	TATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCTCTGCGCACGGTCCGTGCCAGCCA	2647
QY	3211	ATAGATGCTCAGGCTGCGCTCTCCCACTTCACTCAGTTCCCAAACTCTAAATTTTAA	3270
Db	2648	ATAGATGCTCAGGCTGCGCTCTCCCACTTCACTCAGTTCCCAAACTCTAAATTTTAA	2707
QY	3271	CAAGAGATTTCTGTTGGGGGAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCT	3330
Db	2708	CAAGAGATTTCTGTTGGGGGAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCT	2767
QY	3331	GGAAATGTCAATTCCTTAGAAGGAAATTTAGGTTGGTGGAGCAAGCCCCACCTCGGTTT	3390
Db	2768	GGAAATGTCAATTCCTTAGAAGGAAATTTAGGTTGGTGGAGCAAGCCCCACCTCGGTTT	2827
QY	3391	TTCTGCCACAGCATCCAAATCGTGAAGAACTCGGGAGAGGTGGAGTCCACATCTAGGGT	3450
Db	2828	TTCTGCCACAGCATCCAAATCGTGAAGAACTCGGGAGAGGTGGAGTCCACATCTAGGGT	2887
QY	3451	GTCTTCCCTTGGCTCTATCCCTGCCAGAGTGGAACTGGAGAGTGGGGCTGCAAGA	3510
Db	2888	GTCTTCCCTTGGCTCTATCCCTGCCAGAGTGGAACTGGAGAGTGGGGCTGCAAGA	2947
QY	3511	CTGAGCTAAATGTCTCCCGGCTTGAATTTTCTTCTAGTCTCTGGGCTAGATTTCTG	3570
Db	2948	CTGAGCTAAATGTCTCCCGGCTTGAATTTTCTTCTAGTCTCTGGGCTAGATTTCTG	3007
QY	3571	CACTTGGGGTCTTGACACACACACATCCAAAGTAGCCGGAAGAGCTAAACACAGGG	3630
Db	3008	CACTTGGGGTCTTGACACACACACATCCAAAGTAGCCGGAAGAGCTAAACACAGGG	3067
QY	3631	GGTTCTTAAATGGCTGCCCCCGCACCGGGCTCCCTTGGGCAAAAGGAATTTGTACG	3690
Db	3068	GGTTCTTAAATGGCTGCCCCCGCACCGGGCTCCCTTGGGCAAAAGGAATTTGTACG	3127
QY	3691	CCTACCCCAACCTTCAACTACAGAACTTGGGCCACCCCAAGCACTATTTTATTTAAA	3750
Db	3128	CCTACCCCAACCTTCAACTACAGAACTTGGGCCACCCCAAGCACTATTTTATTTAAA	3187
QY	3751	TGTTGCCCATTTTATGAGTTATGATCAATTTGATTAATTAAGTTACAGATGC	3806
Db	3188	TGTTGCCCATTTTATGAGTTATGATCAATTTGATTAATTAAGTTACAGATGC	3243

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 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
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 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
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 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239937P.
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 PR 20-OCT-2000; 2000US-0240960P.
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 PR 01-NOV-2000; 2000US-0244617P.
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 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
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 PR 17-NOV-2000; 2000US-0249214P.
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 PR 17-NOV-2000; 2000US-0249244P.
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 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
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 PR 01-DEC-2000; 2000US-0250160P.
 PR 05-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-02559678P.
 XX
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-483426/52.
 Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and metastasis.
 Disclosure; SEQ ID NO.35436; 307lpp + Sequence Listing; English.
 AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 activity, and can be used in gene therapy and vaccine production. (I)
 proteins and polynucleotides may be used in the prevention, diagnosis and
 treatment of diseases associated with inappropriate (I) expression. For
 example, they may be used to treat disorders associated with decreased
 expression by rectifying mutations or deletions in a patient's genome
 that affect the activity of (I) by expressing inactive proteins or to
 supplement the patient's own production of (I). Additionally, (I)
 polynucleotides may be used to produce the secreted (I), by inserting the
 nucleic acids into a host cell and culturing the cell to express the
 protein. (I) proteins and polynucleotides may be used to prevent,
 diagnose and treat immune/hematopoietic-related diseases, especially
 cancers and cancer metastases of hematopoietic-derived cells. AAK64703

CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 5858 BP; 1455 A; 1579 C; 1490 G; 1334 T; 0 U; 0 Other;
Query Match 60.6%; Score 2319.8; DB 4; Length 5858;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2332; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1473 CCACCCAGTGCACAGCGCCCTAACCCCTGACCCGGGSCACAGCCACAGCGCTGATCCT 1532
DB 1 CCCACAGTGCACAGCGCCCTAACCCCTGACCCGGGSCACAGCCACAGCGCTGATCCT 60
QY 1533 GTCCGACGACTGCACCAATTGTGGCTTACGGCACTTGCACCCACAGCCACTCAGGACTC 1592
DB 61 GTCCGACGACTGCACCAATTGTGGCTTACGGCACTTGCACCCACAGCCACTCAGGACTC 120
QY 1593 GCCAAAGCGCTTCGATGTGGAGGTGTCGGTGTGGTTCCTGAAGCCCTTCAGTAGTGGGT 1652
DB 121 GCCAAAGCGCTTCGATGTGGAGGTGTCGGTGTGGTTCCTGAAGCCCTTCAGTAGTGGGT 180
QY 1653 CCACACTGGGAGGTGGTGGCGGAGAAAGACCCAGTGGGTGATCGGGCTGGCACAGA 1712
DB 181 CCACACTGGGAGGTGGTGGCGGAGAAAGACCCAGTGGGTGATCGGGCTGGCACAGA 240
QY 1713 AGCCGACGCGAAGGGGAGCATCCAGATCCAGCCACAGCCCGGGTTCCTACTGCATCGT 1772
DB 241 AGCCGACGCGAAGGGGAGCATCCAGATCCAGCCACAGCCCGGGTTCCTACTGCATCGT 300
QY 1773 GATGCACGATGCAACCACTGACAGCCCTGACGGAGCCCTGGACCGCTTAACTCCG 1832
DB 301 GATGCACGATGCAACCACTGACAGCCCTGACGGAGCCCTGGACCGCTTAACTCCG 360
QY 1833 GGAACGCTTGAACAGGTGGGTGTCTTCTCGACTATGACCAAGGCTTCTCATCTTCTA 1892
DB 361 GGAACGCTTGAACAGGTGGGTGTCTTCTCGACTATGACCAAGGCTTCTCATCTTCTA 420
QY 1893 CAATGCTGATGATGTCTTGCTGTACACCTTCGGGAGAGTTCCTGGCAGCTCTG 1952
DB 421 CAATGCTGATGATGTCTTGCTGTACACCTTCGGGAGAGTTCCTGGCAGCTCTG 480
QY 1953 CTCTTACTTTCAGCCCTGGCCAGAGCCACGCCAATGCAAGAGCTTCAGCCGCTGGGAT 2012
DB 481 CTCTTACTTTCAGCCCTGGCCAGAGCCACGCCAATGCAAGAGCTTCAGCCGCTGGGAT 540
QY 2013 CAACACCGTCCGATCTAGTCCAGGAGAGGAGACCAACCTCTCGGACCACTGCCA 2072
DB 541 CAACACCGTCCGATCTAGTCCAGGAGAGGAGACCAACCTCTCGGACCACTGCCA 600
QY 2073 CCTGCAAGAGCCCTGCCAGGAGATAGAGACCTGGACTCCAGCCACCGTGGCCACTG 2132
DB 601 CCTGCAAGAGCCCTGCCAGG-AGATAGAGACCTGGACTCCAGCCACCGTGGCCACTG 659
QY 2133 GAGACCTCAGGCGAGTGTGTACCTCCAGCCCTCAGCTCTGTAAATAGGAGTTCGATTC 2192
DB 660 GAGACCTCAGGCGAGTGTGTACCTCCAGCCCTCAGCTCTGTAAATAGGAGTTCGATTC 719
QY 2193 CTCTACTTCTAACTCTCTTCACAGATGATGTTGTGTAGCTCTGACCTGTGATAGGATA 2252
DB 720 CTCTACTTCTAACTCTCTTCACAGATGATGTTGTGTAGCTCTGACCTGTGATAGGATA 779
QY 2253 GAGCTTTGATCCAGAGATGATGATGGCTTCCTCAGGGCAACCCCTGCCAACCCCTCA 2312
DB 780 GAGCTTTGATCCAGAGATGATGATGGCTTCCTCAGGGCAACCCCTGCCAACCCCTCA 839
QY 2313 TCCCATCTTCTCAGGGGAGGGGACTACTCTTCAGTGTCTCCTCAGCCACGCGCTTGA 2372
DB 840 TCCCATCTTCTCAGGGGAGGGGACTACTCTTCAGTGTCTCCTCAGCCACGCGCTTGA 899
QY 2373 CTTGAGAAAGTGTACAGCATGGCCAGTAGTGTGGAGCCGGAAGACACACAGCACCTTC 2432
DB 900 CTTGAGAAAGTGTACAGCATGGCCAGTAGTGTGGAGCCGGAAGACACACAGCACCTTC 959

QY 2433 TTATGTCCCATGGCCCTAAGACTTACCCCTGACCAAGCTAGTGTATGGGCCATTTACCCCTTG 2492
DB 960 TTATGTCCCATGGCCCTAAGACTTACCCCTGACCAAGCTAGTGTATGGGCCATTTACCCCTTG 1019
QY 2493 ACCCCAGTCCACAGTGGTTCACAGGTAGTACCTGGTCTCCTAGGTTGGCTCAGAGCCAACT 2552
DB 1020 ACCCCAGTCCACAGTGGTTCACAGGTAGTACCTGGTCTCCTAGGTTGGCTCAGAGCCAACT 1079
QY 2553 CTCCTGCCACCCCCACACCAAGAACTATATGGTTCTTACTTCTCCCACTGATCTGCTGTG 2612
DB 1080 CTCCTGCCACCCCCACACCAAGAACTATATGGTTCTTACTTCTCCCACTGATCTGCTGTG 1139
QY 2613 CAGTGTATGTCTGTGGCTGTGGAGGCACTGTGTAGTGTAGTCCACATATATGTCTA 2672
DB 1140 CAGTGTATGTCTGTGGCTGTGGAGGCACTGTGTAGTGTAGTCCACATATATGTCTA 1199
QY 2673 TGTGCCACCACTTCTCTGCCCA CAGGCCGAGGGA CAGGGTGAGGGTATATACCCAAAGCTCA 2732
DB 1200 TGTGCCACCACTTCTCTGCCCA CAGGCCGAGGGA CAGGGTGAGGGTATATACCCAAAGCTCA 1259
QY 2733 TGCAGAGCCCACTTAGCTTAAAGCAACTGCAAGCAAGCTCCCTGGATGATCGAGGTCC 2792
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QY 2793 CCACTAGCTCTGAA CAAGAGTCCAGCAACCTCTTCCAGCAGGCTCTCTGCACCTGCTA 2852
DB 1320 CCACTAGCTCTGAA CAAGAGTCCAGCAACCTCTTCCAGCAGGCTCTCTGCACCTGCTA 1379
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DB 1380 GGGTGCAGGAGCTTCCAGAAAGCAGTGTGTAAATTAGGACCAAGCACTGGGAGGGGT 1439
QY 2913 GTTGGCTAGACCCCTTGTGATCTTGGGCACTATCTCACTTAGGATCTCTGCTGCAAAAA 2972
DB 1440 GTTGGCTAGACCCCTTGTGATCTTGGGCACTATCTCACTTAGGATCTCTGCTGCAAAAA 1499
QY 2973 CAAGAGCCACTTGTAGCTGGTTTAAATAGCAAGGATTTACTACCTGGCCCTGGTGGCT 3032
DB 1500 CAAGAGCCACTTGTAGCTGGTTTAAATAGCAAGGATTTACTACCTGGCCCTGGTGGCT 1559
QY 3033 TGCAAAATTTGTGGAGAGCTGGGAAAGCAGACTCTGCTGAAATTTCCAGGAACTCCCAAG 3092
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QY 3093 GCCAGATTCACTCATGTCTGTTGTGACCCAGGAAAGCTGCCCCCATCTGCAAGGAGCCACTA 3152
DB 1620 GCCAGATTCACTCATGTCTGTTGTGACCCAGGAAAGCTGCCCCCATCTGCAAGGAGCCACTA 1679
QY 3153 TGCAGAAAGCTGTGACTGCAAGAACTAGGCTCCCTCTGCCAGGTCCTGCGCAGCCAAAT 3212
DB 1680 TGCAGAAAGCTGTGACTGCAAGAACTAGGCTCCCTCTGCCAGGTCCTGCGCAGCCAAAT 1739
QY 3213 AGATGCTCTGAGGCTGCCCCCTCTCCCACTTCACTCAGTTCCTCAAAATCTAAATTTTACA 3272
DB 1740 AGATGCTCTGAGGCTGCCCCCTCTCCCACTTCACTCAGTTCCTCAAAATCTAAATTTTACA 1799
QY 3273 AGAGATTCTGTTTGGGGGAACTTAAGTCAAGTCCAGAACTTGGCTGCGTCAAGGAGTCTGG 3332
DB 1800 AGAGATTCTGTTTGGGGGAACTTAAGTCAAGTCCAGAACTTGGCTGCGTCAAGGAGTCTGG 1859
QY 3333 GAAATGTCAATTTCCCTAGAGGAAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTTTT 3392
DB 1860 GAAATGTCAATTTCCCTAGAGGAAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTTTT 1919
QY 3393 CTGCCACAGCATCCAATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGTTGT 3452
DB 1920 CTGCCACAGCATCCAATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGTTGT 1979
QY 3453 CTGCGCCCTTGGCTCTATCCCTGCGCAGAGTGGGAACTGAGGAGTGGGCTGCAAGACT 3512
DB 1980 CTGCGCCCTTGGCTCTATCCCTGCGCAGAGGTGGGAACTGAGGAGTGGGCTGCAAGACT 2039

QY 3513 GAGCTAAATGTCTCCCGGCTTGAATTTCTTTCTAGTCTGGGGCTTAGATTTCTGCA 3572
Db |||||
QY 2040 GAGCTAAATGTCTCCCGGCTTGAATTTCTTTCTAGTCTGGGGCTTAGATTTCTGCA 2099
Db |||||
QY 3573 CTTGGGCTCTTGACACACACACACCATCCCAAAGTAGCCGGAAGAGCTAAACACAGGGGG 3632
Db CTTGGGCTCTTGACACACACACACCATCCCAAAGTAGCCGGAAGAGCTAAACACAGGGGG 2159
QY 3633 TTCTTAAATGGTGGCCCGCCACCGGGCTCCCTTGGGCAAAAGAAATGTCAGCCC 3692
Db TTCTTAAATGGTGGCCCGCCACCGGGCTCCCTTGGGCAAAAGAAATGTCAGCCC 2219
QY 3693 TACCCCAACCTTCAACTACAGAACTCTGGGCCACCCAGCAGTATTTTATTAAATG 3752
Db TACCCCAACCTTCAACTACAGAACTCTGGGCCACCCAGCAGTATTTTATTAAATG 2279
QY 3753 TTGCCCAATTTATGAGTTATGATCAATTTGTTATTAATTTAAAGTTACAGATGTCA 3807
Db TTGCCCAATTTATGAGTTATGATCAATTTGTTATTAATTTAAAGTTACAGATGTCA 2334

RESULT 6
ABK12811
ID ABK12811 standard; DNA; 30676 BP.
AC ABK12811;
XX
XX
DT 18-JUN-2002 (first entry)
XX
XX Human tumour suppressor CAR-1, BAC clone RP11-131M11.
XX
XX Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteriophage artificial chromosome; chromosome 1p31-1p36.
XX
XX Homo sapiens.
XX
XX WO200212285-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025269.
XX
XX 10-AUG-2000; 2000US-0225033P.
XX
XX 23-AUG-2000; 2000US-0227560P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Killary A, Chandler D, Lott S;
XX
XX WPI; 2002-269088/31.
XX
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
XX Disclosure; Page 176-185; 185pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating

CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene
XX

SQ Sequence 30676 BP; 7591 A; 7621 C; 7888 G; 6944 T; 0 U; 632 Other;
Query Match 60.3%; Score 2308.6; DB 6; Length 30676;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2348; Conservative 0; Mismatches 29; Indels 2; Gaps 2;
QY 1429 GGCCCTCGCAGTACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCAGTCCGAGCC 1488
Db 23371 GGTTCCACAGCCTTCTCCCACTCATCTTCTCTCCCTCTCCAAACCCACAGTCCGAGCC 23430
QY 1489 GCCTTAACCTGGACCCGGGACAGCCACAGCGCTGATCTCTGGAGCATGTCGACC 1548
Db 23431 GCCTTAACCTGGACCCGGGACAGCCACAGCGCTGATCTCTGGAGCATGTCGACC 23490
QY 1549 ATTGTGCTTTACGGCAACTTTGCCACCCACAGCCTGTCAGGACTGCGCAAGCGCTTCGAT 1608
Db 23491 ATTGTGCTTTACGGCAACTTTGCCACCCACAGCCTGTCAGGACTGCGCAAGCGCTTCGAT 23550
QY 1609 GTGAGGTGTCGGTGTCTGGGTCTGGAAGCTTTCAGTAGTGGCTGCTCACTACTGGAGGTG 1668
Db 23551 GTGAGGTGTCGGTGTCTGGGTCTTCTGAAGCCTTTCAGTAGTGGCTGCTCACTACTGGAGGTG 23610
QY 1669 GTGTGGCGGAGAAAGACCCAGTGGGTGATCGGGTGGCACACGAAGCCGCAAGCCGAAG 1728
Db 23611 GTGTGGCGGAGAAAGACCCAGTGGGTGATCGGGTGGCACACGAAGCCGCAAGCCGAAG 23669
QY 1729 GGCAGCATCCAGATCCAGCCCGCGGCTTCTACTGTCATCGTGTGATGTCAGATGGCAAC 1788
Db 23670 GGCAGCATCCAGATCCAGCCCGCGGCTTCTACTGTCATCGTGTGATGTCAGATGGCAAC 23729
QY 1789 CAGTACAGCGCTTCGACGAGAGCCCTGGACGGGCTTAACCTCCGGGACAGCTTGCAAG 1848
Db 23730 CAGTACAGCGCTTCGACGAGAGCCCTGGACGGGCTTAACTCCGGGACAGCTTGCAAG 23789
QY 1849 GTGGGTGTCCTCTGGACTATGACCAAGGCTTGCTCATCTTCTACATGCTGATGACATG 1908
Db 23790 GTGGGTGTCCTCTGGACTATGACCAAGGCTTGCTCATCTTCTACATGCTGATGACATG 23849
QY 1909 TCTGGCTCTACACCTTCCCGGAGAGTTCCTCGGCAAGCTCTGCTCTTACTTCAGGCCT 1968
Db 23850 TCTGGCTCTACACCTTCCCGGAGAGTTCCTCGGCAAGCTCTGCTCTTACTTCAGGCCT 23909
QY 1969 GGCACAGGCCACCCCAATGCAAGAGCTTCAGCCGCTGGGATCAACACGTCGCGATC 2028
Db 23910 GGCACAGGCCACCCCAATGCAAGAGCTTCAGCCGCTGGGATCAACACGTCGCGATC 23969

QY 2029 TAGTCCAGGAGAGGAGACACACACCTCTCGGGACCACTGCCACCTGCAAGAGCCCTGC 2088
DB 23970 TAGTCCAGGAGAGGAGACACACACCTCTCGGGACCACTGCCACCTGCAAGAGCCCTGC 24029
QY 2089 CCAGGAAGATAGAGACCTGGACTCCAGCCCAACCGTGGCCACTGGAGACCTCAGGCCAGT 2148
DB 24030 CCAGG-AGATAGAGAACCTGGACTCCAGCCCAACCGTGGCCACTGGAGACCTCAGGCCAGT 24088
QY 2149 TGTATTACCTCCAGCCTCAGTCTGTGTAAATGGAGGTTGCATTCCTACTTCTTAACTC 2208
DB 24089 TGTATTACCTCCAGCCTCAGTCTGTGTAAATGGAGGTTGCATTCCTACTTCTTAACTC 24148
QY 2209 TCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCTTTGATCCAGG 2268
DB 24149 TCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCTTTGATCCAGG 24208
QY 2269 ATGTGACATGGTCTCTCTCAGGGCAACCCCTGCCCAACCCCTCATCCCCATCTTCTCAGG 2328
DB 24209 ATGTGACATGGTCTCTCTCAGGGCAACCCCTGCCCAACCCCTCATCCCCATCTTCTCAGG 24268
QY 2329 GGCAGGGACATACCTTCCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTAG 2388
DB 24269 GGCAGGGACATACCTTCCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTAG 24328
QY 2389 AGCATGGCCAGTGTGGCAGCCCGAAAGACACACAGCACCTCTTATGTCCCATGGCT 2448
DB 24329 AGCATGGCCAGTGTGGCAGCCCGAAAGACACACAGCACCTCTTATGTCCCATGGCT 24388
QY 2449 AAGACTTACCCCTGACCAAGCTAGTGTAGGGCCATTACCCCTGACCCCAAGTCCACAGTG 2508
DB 24389 AAGACTTACCCCTGACCAAGCTAGTGTAGGGCCATTACCCCTGACCCCAAGTCCACAGTG 24448
QY 2509 GTCCAGAGTGTACCTGTCTAGGGTTCCTGAGGACCACTCTCTGACACCCCTC 2568
DB 24449 GTCCAGAGTGTACCTGTCTAGGGTTCCTGAGGACCACTCTCTGACACCCCTC 24508
QY 2569 ACCAAGACTATATGTTCTACTTCTCCACTGTCTGCTGATGATGATGATGATG 2628
DB 24509 ACCAAGACTATATGTTCTACTTCTCCACTGTCTGCTGATGATGATGATGATG 24568
QY 2629 GCTGTGGAAGCACCTGTTAGTGTAGTCCACACATTATAGTGTGACCACTTCC 2688
DB 24569 GCTGTGGAAGCACCTGTTAGTGTAGTCCACACATTATAGTGTGACCACTTCC 24628
QY 2689 TSCCCACAGCCGAGGACAGGTTAGGTTATACCAAGCTGTGATGACAGGCCATTAGC 2748
DB 24629 TSCCCACAGCCGAGGACAGGTTAGGTTATACCAAGCTGTGATGACAGGCCATTAGC 24688
QY 2749 CTAAAGCAACTGCAGGACCAAGCCTCCCTGGATGATCGAGGTCCCGAGTGTCTGAACA 2808
DB 24689 CTAAAGCAACTGCAGGACCAAGCCTCCCTGGATGATCGAGGTCCCGAGTGTCTGAACA 24748
QY 2809 AGAGTCCAGCCCAACCTCTTACGCCAGGCTCTGTGACCTGTAGGGTGCAGAGGCTTC 2868
DB 24749 AGAGTCCAGCCCAACCTCTTACGCCAGGCTCTGTGACCTGTAGGGTGCAGAGGCTTC 24808
QY 2869 CAGAAGCAGTGTGTAAATAGGACCAAGCACTGGAGGGCTGTGCTAGACCCCTT 2928
DB 24809 CAGAAGCAGTGTGTAAATAGGACCAAGCACTGGAGGGCTGTGCTAGACCCCTT 24868
QY 2929 GTCCAGCTTGGCATCTATCTCAGTTAGGATCTGCTGCAGAAACCAAGAGCCACTGTAG 2988
DB 24869 GTCCAGCTTGGCATCTATCTCAGTTAGGATCTGCTGCAGAAACCAAGAGCCACTGTAG 24928
QY 2989 CTGGTTTAAATTAGCAAGGATTTACTCTGGCCCTGTGGCTTGCATAAATTTGTGGAA 3048
DB 24929 CTGGTTTAAATTAGCAAGGATTTACTCTGGCCCTGTGGCTTGCATAAATTTGTGGAA 24988
QY 3049 GAGCTGGAGACAGACTCTGCTGAATTTCCAGGAATCTCCAGCGCCAGATTCATCATGT 3108
DB 24989 GAGCTGGAGACAGACTCTGCTGAATTTCCAGGAATCTCCAGCGCCAGATTCATCATGT 25048
QY 3109 CTGTTGTGACCAAGAAAGCTGCCCCATCTGTCAGGAAGCACTATGCCAGAAAGCTGCTG 3168

DB 25049 CTGTTGTGACAGAAAGCTGCCCCATCTGCAGGAAGCCACTATGCCAAGAAAGCTGCTG 25108
QY 3169 ACTGCAGAACTAGGCTCCCTCTGCGACCGTTCGTCGCCAGCAATAGATGTCTGAGGCT 3228
DB 25109 ACTGCAGAACTAGGCTCCCTCTGCGACCGTTCGTCGCCAGCAATAGATGTCTGAGGCT 25168
QY 3229 GCCCTCTCCCACTTCACTCAGTTCCTCCAAATCTAAATTTTACAAGAGATCTGTTGGG 3288
DB 25169 GCCCTCTCCCACTTCACTCAGTTCCTCCAAATCTAAATTTTACAAGAGATCTGTTGGG 25228
QY 3289 GGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGTCAATTCCT 3348
DB 25229 GGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGTCAATTCCT 25288
QY 3349 AGAAGAAAGTTAGGTTGGTGGAGCAAGCCCACTGCGTTTTTCTGCCACAGATCCAA 3408
DB 25289 AGAAGAAAGTTAGGTTGGTGGAGCAAGCCCACTGCGTTTTTCTGCCACAGATCCAA 25348
QY 3409 TCGTGAAGAACTCGGAGAGGTTGAGTCCACATCTAGGTTGTCTGCCCTTGGCTCT 3468
DB 25349 TCGTGAAGAACTCGGAGAGGTTGAGTCCACATCTAGGTTGTCTGCCCTTGGCTCT 25408
QY 3469 ATCCCTGCGCCAGAGGTGGGAACCTGGAGGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCC 3528
DB 25409 ATCCCTGCGCCAGAGGTGGGAACCTGGAGGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCC 25468
QY 3529 CCGGCTGTGACTTTTCTTTAGTCTCTGGGCTAGATTCTGCACTTGGGGTCTCTGACA 3588
DB 25469 CCGGCTGTGACTTTTCTTTAGTCTCTGGGCTAGATTCTGCACTTGGGGTCTCTGACA 25528
QY 3589 CACACACCTCCCAAGTAGCCGGAAGACTAAACACAGGGGTTCTTAAATGGCTC 3648
DB 25529 CACACACCTCCCAAGTAGCCGGAAGACTAAACACAGGGGTTCTTAAATGGCTC 25588
QY 3649 CCCCCGCCACCCGGGCTCTCCCTTGGGCAAAAGAAATTGTGAGCCCTACCCCAACCCCTCAA 3708
DB 25589 CCCCCGCCACCCGGGCTCTCCCTTGGGCAAAAGAAATTGTGAGCCCTACCCCAACCCCTCAA 25648
QY 3709 CTACAGAACTCTGGGCCACCCCGAGCAGTATTTTATTTAAATGTGGCCATTTTATGAG 3768
DB 25649 CTACAGAACTCTGGGCCACCCCGAGCAGTATTTTATTTAAATGTGGCCATTTTATGAG 25708
QY 3769 TTATCATCAATTTGTATTAATTAAGTTACAGATGTCA 3807
DB 25709 TTATCATCAATTTGTATTAATTAAGTTACAGATGTCA 25747

RESULT 7
AAK80625
ID AAK80625 standard; DNA; 5866 BP.
XX
AC AAK80625;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35437.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US0001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.
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PR 07-JUN-2000; 2000US-0209467P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 35437; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients' own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 5866 BP; 1464 A; 1580 C; 1489 G; 1333 T; 0 U; 0 Other;

Query Match 60.3%; Score 2306.2; DB 4; Length 5866;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2330; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 1473 CCACCAGTGCAGCGCCCTAACCTGGACCGCGGCACAGCCACAGCGCCTGATCCT 1532
DB 1 CCCACAGTGCAGCGCCCTAACCTGGACCGCGGCACAGCCACAGCGCCTGATCCT 60
QY 1533 GTCGACGACGTGCACCATTTGGCTTACGGCAACTTGCACCCACAGCCACTCAGGACTC 1592
DB 61 GTCGACGACGTGCACCATTTGGCTTACGGCAACTTGCACCCACAGCCACTCAGGACTC 120
QY 1593 GCCAAGCGCTTCGATGTGGAGGTGTGGTGTGGTTCGAGCCTTCAGTAGTGGGT 1652
DB 121 GCCAAGCGCTTCGATGTGGAGGTGTGGTGTGGTTCGAGCCTTCAGTAGTGGGT 180
QY 1653 CCACCTACTGGAGGTGGTGTGGCGAGAGACCCAGTGGGTGATCGGCTCGCACAGA 1712
DB 181 CCACCTACTGGAGGTGGTGTGGCGAGAGAGACCCAGTGGGTGATCGGCTCGCACAGA 240
QY 1713 AGCCGCAAGCCGCAAGGGCAGCATCCAGATCCAGCCCGACCGCGCTTCTACTGATCGT 1772
DB 241 AGCCGCAAGCCGCAA-GGCAGCATCCAGATCCAGCCCGACCGCGCTTCTACTGATCGT 299
QY 1773 GATGACGATGCAACCACTAGTACGCGCTGCAGGAGCCCTGCAGCGGCTTAACTCGG 1832
DB 300 GATGACGATGCAACCACTAGTACGCGCTGCAGGAGCCCTGCAGCGGCTTAACTCGG 359
QY 1833 GGACAAAGCTTGACAGGTGGGTGTCTTCTGGACTATGACCAAGGCTTGTCTCATCTTCTA 1892
DB 360 GGACAAAGCTTGACAGGTGGGTGTCTTCTGGACTATGACCAAGGCTTGTCTCATCTTCTA 419
QY 1893 CAATGCTGATGACATGTCTGTGCTCTACACCTTCCGCGAGAGTTCCTTGGCAAGCTGTG 1952
DB 420 CAATGCTGATGACATGTCTGTGCTCTACACCTTCCGCGAGAGTTCCTTGGCAAGCTGTG 479
QY 1953 CTCCTTACTTCAGCCCTGGCCAGCCAGCCCAATGCGAAGACGTTTCAGCCCTCGGGAT 2012
DB 480 CTCCTTACTTCAGCCCTGGCCAGCCAGCCCAATGCGAAGACGTTTCAGCCCTCGGGAT 539
QY 2013 CAACACCGTCCGACATCTAGTCCAGGAGAGGAGACCAAACTCTCTGGGACCACTTGCCA 2072
DB 540 CAACACCGTCCGACATCTAGTCCAGGAGAGGAGACCAAACTCTCTGGGACCACTTGCCA 599
QY 2073 CTTGCAAGACCGCTGCCAGGAGATAGAAAGACCTTGGATCCAGGCCCACTGGGCCACTG 2132
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QY 2253 CAGCTTTGATCCAGGATGTGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCTCA 2312
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DB 839 TCCCATCTTCTCAGGGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGA 898
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QY 2433 TTAATGCCATCTTCCAGTGTGATCTACCTTCCAGTGTGATGGGCTTATACCTTGT 2492
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QY 2493 ACCCCAGTCCACAGTGTTCACAGGTAGTACCTGGTCTCTAGGTTCCCTGAGAGCCAACT 2552
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QY 2553 CTCTTGCACCCCCACACCAAGAACTATATGGTTCCTTCTCTCCACTGATCTCTGTGT 2612
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QY 2673 TGTGCCACACCTTCTCTCCACAGGCGAGGAGGAGGTAGGTATACCCAAAGCTGA 2732
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QY 3333 GAAATGTCATTTCCTAGAGGAGTTAGGTGGTGGAGCAAGCCCACTGGTTTTT 3392
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Db |
QY 3393 CTGCGACAGCATCAATCGTGAAGAACTCGGGAGAGGGTGAGTCCACATCTAGGGTTGT 3452
Db |
QY 1919 CTGCGACAGCATCAATCGTGAAGAACTCGGGAGAGGGTGAGTCCACATCTAGGGTTGT 1978
QY 3453 CCTGCCCCCTGGTCTATCTCCTGCCAGAGTGGGAACTGGAGAGTGGCTGCAAGACT 3512
Db |
QY 1979 CCTGCCCCCTGGTCTATCTCCTGCCAGAGTGGGAACTGGAGAGTGGCTGCAAGACT 2038
QY 3513 GAGCTAAATGTCTCCCGGCTTGACTTTTCTTAGTCTCTGGGGCTAGATTCTGCA 3572
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Db |
QY 2099 CTGCGGGTCTTGACACAAACACCATCCCAAGTAGTACCGGAGAGCTAAACACAGGGG 2158
QY 3633 TTCTTAAATGGTGGTCCCGGCTCCCGGCTCCCTTGGGCAAGAGGAAATTCAGCCC 3692
Db |
QY 2159 TTCTTAAATGGTGGTCCCGGCTCCCGGCTCCCTTGGGCAAGAGGAAATTCAGCCC 2218
QY 3693 TACCCCAACCTTCAACTACCAGAACTCTGGGCCACCCAGCAGTAATTTTATTAAATG 3752
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QY 2219 TACCCCAACCTTCAACTACCAGAACTCTGGGCCACCCAGCAGTAATTTTATTAAATG 2278
QY 3753 TTGCCCAATTTATGAGTTATGATCAATTTGTTATTAATTAAGTTACAGATGCA 3807
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RESULT 8

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ABK12808
ID ABK12808 standard; DNA; 30625 BP.
XX
AC ABK12808;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor CAR-1, BAC clone 392H05 3' sequence.
XX
KW Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteriophage artificial chromosome; chromosome 1p31-1p36.
XX
OS Homo sapiens.
XX
PN WO200212285-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
PR 10-AUG-2000; 2000US-0225033P.
XX
PR 23-AUG-2000; 2000US-0227560P.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Killary A, Chandler D, Lott S;
XX
XX WPI; 2002-269088/31.
XX
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
XX diagnosing cancer, for altering the phenotype of a tumor cell, for
XX treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
XX Disclosure; Page 149-157; 185pp; English.
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CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC non-transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene
XX
XX SQ Sequence 30625 BP; 8084 A; 7712 C; 7487 G; 7314 T; 0 U; 28 Other;
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Query Match 58.9%; Score 2252.8; DB 6; Length 30625;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 57; Indels 3; Gaps 3;
QY 1429 GGGCCCTCGAGTACACATCTGGAAAGTCCCTCTTCAGAGACATCCACCCAGTGCACGCC 1488
Db |
QY 21906 GGTCCACACCCCTTCTCCCACTCATCTCTCTCCCTCTCCAAACCCCAACAGTGCACGCC 21965
Db |
QY 1489 GGCCTAACCTGGACCCGGGACAGCCACAGCCACTGCAGGACTTCGCAAGCGCTTCGAT 1508
Db |
QY 21966 GGCCTAACCTGGACCCGGGACAGCCACAGCCACTGCAGGACTTCGCAAGCGCTTCGAT 22025
QY 1549 ATTGTGGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTTCGCAAGCGCTTCGAT 1508
Db |
QY 22026 ATTGTGGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTTCGCAAGCGCTTCGAT 22085
QY 1609 GTGGAGGTGTGGTGTGGTCTTGAAGCCCTTCAGTGTGGCTTCCTACTCTGGAGGTG 1668
Db |
QY 22086 GTGGAGGTGTGGTGTGGTCTTGAAGCCCTTCAGTGTGGCTTCCTACTCTGGAGGTG 22145
QY 1669 GTGGTGGCGGAGAGCCAGTGGGTGATCGGGCTGGCAACAGCCAGCCGCGCAAG 1728
Db |
QY 22146 GTGGTGGCGGAGAGAGCCAGTGGGTGATCGGGCTGGCAACAGCCGCGCGCAAG 22205
QY 1729 GGCAGCATCCAGATCCAGCCCGCGGCTTCTACTGTCATCGTGTGATGCGATGGCAAC 1788
Db |
QY 22206 GGCAGCATCCAAATCCAGCCCGCGGCTTCTACTGTCATCGTGTGATGCGATGGCAAC 22265
QY 1789 CAGTACAGCGCTTCAGCGGAGCCCTCGACCGGCTTAACTCCGGGACAGCTTGCAAG 1848
Db |
QY 22266 CAGTACAGCGCTTCAGCGGAGCCCTCGACCGGCTTAACTCCGGGACAGCTTGCAAG 22325
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Db 667 GACCGGTGAGCTGGGTGCGAGCATTTCTTCTGCGCGCTGATCACGGAGCACTGG 726
QY 721 GTGCGGAGGAGCGCAGGGGCCCGCGACTGCCCGAGTCCGCGCGACGTTCCCGGAG 780
Db 727 GTGCGGAGGAGCGCAGGGGCCCGCGACTGCCCGAGTCCGCGCGACGTTCCCGGAG 786
QY 781 CCGCGCTGGCGCCAGACCTCAAGCTGGCAACATGTTGGAGGGCTACAGCTTCCTTCCG 840
Db 787 CCGCGCTGGCGCCAGACCTCAAGCTGGCAACATGTTGGAGGGCTACAGCTTCCTTCCG 846
QY 841 CTGGAGCGCCATCTCAACGCGCGCGCGCGGCGGACCTTGCAGCGCGACGACCAAGGTC 900
Db 847 CTGGAGCGCCATCTCAACGCGCGCGCGCGGCGGACCTTGCAGCGCGACGACCAAGGTC 906
QY 901 AAGCTCTTCTGCTCACGACCGCGCGCTTCTGCTTCTTCTGCGACGAGCTGCACTG 960
Db 907 AAGCTCTTCTGCTCACGACCGCGCGCTTCTGCTTCTTCTGCGACGAGCTGCACTG 966
QY 961 CAGGAGCAGCATAGTTCACCGGCTCGAGCGGCTTTCGAGAGCTGCAGGGAGCTG 1020
Db 967 CAGGAGCAGCATAGTTCACCGGCTCGAGCGGCTTTCGAGAGCTGCAGGGAGCTG 1026
QY 1021 AAGGACCAACTTCAGGCCCTTCAAGACGAGCGGGAAACACACGAAGCGCTGCAGCTG 1080
Db 1027 AAGGACCAACTTCAGGCCCTTCAAGACGAGCGGGAAACACACGAAGCGCTGCAGCTG 1086
QY 1081 CTCAGCGCAAACTGGCGGAGACCAAGTCTTCCACGAGAGCTGCGGACCACTATCGCG 1140
Db 1087 CTCAGCGCAAACTGGCGGAGACCAAGTCTTCCACGAGAGCTGCGGACCACTATCGCG 1146
QY 1141 GAGGCTTTGAGGGGTGACCGGCTGCTGGTGAACGCGCAGAGGCGATGCTAGAGGAG 1200
Db 1147 GAGGCTTTGAGGGGTGACCGGCTGCTGGTGAACGCGCAGAGGCGATGCTAGAGGAG 1206
QY 1201 CTGGAGGGGACACGCGCGCGCTGACCGCATCGGACATCGAGCAAGTCCAGCGCTACAGC 1260
Db 1207 CTGGAGGGGGAACGCGCGCGCTGACCGCATCGGACATCGAGCAAGTCCAGCGCTACAGC 1266
QY 1261 CAGGAGCTGCGAAGTTCAGAGGGAGGAGCCGAGATCTCTGAGAGGCGGTGCTGAAACC 1320
Db 1267 CAGGAGCTGCGAAGTTCAGAGGGAGGAGCCGAGATCTCTGAGAGGCGGTGCTGAAACC 1326
QY 1321 GACCGGCACACCTTCCTGGCTGGGTGGCTCACTGTCCGCGGCTCAAGGGAAATTC 1380
Db 1327 GACCGGCACACCTTCCTGGCTGGGTGGCTCACTGTCCGCGGCTCAAGGGAAATTC 1386
QY 1381 CATGAGACCAACTCACATATGAAGACTTCCCGACCTCCAAAGTACACAGGCCCCCTGCGAG 1440
Db 1387 CATGAGACCAACTCACATATGAAGACTTCCCGACCTCCAAAGTACACAGGCCCCCTGCGAG 1446
QY 1441 TACACATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCAGCGCCCTTAACCTTG 1500
Db 1447 TACACATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCAGCGCCCTTAACCTTG 1506
QY 1501 GACCGGGCAGACGCCACAGCGCCTGATCTGTGCGAGCTGCACCAATGTGGCTTAC 1560
Db 1507 GACCGGGCAGACGCCACAGCGCCTGATCTGTGCGAGCTGCACCAATGTGGCTTAC 1566
QY 1561 GGCNACTTCACCCACAGCCACTGCAGGACTCGCCAAAGCGCTTCGATGTGAGGTGTG 1620
Db 1567 GGCNACTTCACCCACAGCCACTGCAGGACTCGCCAAAGCGCTTCGATGTGAGGTGTG 1626
QY 1621 GTGCTGGGTTCTGAAGCTTCAGTAGTGGGTTCCTACTGTGGAGGTGTGTGGCGGAG 1680
Db 1627 GTGCTGGGTTCTGAAGCTTCAGTAGTGGGTTCCTACTGTGGAGGTGTGTGGCGGAG 1686
QY 1681 AAGACCCAGTGGTGTATCGGGCTGGCACACGAGCGCGAAGCGGAGGCGAGCATCCAG 1740
Db 1687 AAGACCCAGTGGTGTATCGGGCTGGCACACGAGCGCGAAGCGGAGGCGAGCATCCAG 1746
QY 1741 ATCCAGCCAGCGCGCGC 1758
```

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Db 1747 ATCCAGAACCTTGGCTGC 1764

RESULT 11
ADC37454
ID ADC37454 standard; DNA; 2207 BP.
XX
AC ADC37454;
XX
DT 18-DEC-2003 (first entry)
XX
DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 287.
XX
KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
cancer; infectious disease; bone disease; AIDS;
neurodegenerative disease; ischaemic disorder; Antinflammatory;
Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003048202-A2.
XX
PD 12-JUN-2003.
XX
PF 03-DEC-2002; 2002WO-JP012644.
XX
PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX
PA (ASAH ) ASahi KASEI KK.
XX
PI Matsuda A, Muramatsu S;
XX
WPI: 2003-505282/47.
P-PSDB; ADC37455.
XX
New purified protein that activates nuclear factor kappa B (NF-kappaB),
useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
PS Claim 4; SEQ ID NO 287; 938pp; English.
XX
The present invention relates to novel proteins and their coding
sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
kappaB). The proteins and their coding sequences are useful for treating
a disease associated with NF-kappaB activation, such as inflammation,
autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
neurodegenerative diseases, or ischaemic disorders.
XX
SQ Sequence 2207 BP; 414 A; 784 C; 618 G; 391 T; 0 U; 0 Other;

Query Match 43.3%; Score 1657.2; DB 9; Length 2207;
Best Local Similarity 97.3%; Pred. No. 5e-307;
Matches 1711; Conservative 0; Mismatches 8; Indels 39; Gaps 1;

QY 1 AGGCTGCGCTGGACCAAGCGGTGCTGCTAAGCTCGCGGGGTAAAGGGTGCAGTGGG 60
Db 7 AGGCTGCGCTGGACCAAGCGGTGCTGCTAAGCTCGCGGGGTAAAGGGTGCAGTGGG 66
QY 61 CAGAGGTTTGGGCGCGGATCCGGAGCTGAGCGGCGCGGACCCCTCTCTTCTGCTGCC 120
Db 67 CCAGGGTTTGGGCGCGGATCCGGAGCTGAGCGGCGCGGACCCCTCTCTTCTGCTGCC 126
QY 121 GGTCTACAGCCATGTACGCTCGGCTCGGCTCGCCCTCCCGCAGATTCCCATCCCCA 180
Db 127 GGTCTACAGCCATGTACGCTCGGCTCGGCTCGCCCTCCCGCAGATTCCCATCCCCA 186
QY 181 GCTTCTCGCCCTCCCGCAGCCGCCCCACCCCGGGATTTCGACCCCTTTAAGGGTCCAC 240
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Db 187 GCTTCTCGCCCTCCCGCAGCCGCCCAACCCCGGATTTTCGACCCCTTAAGGCTCCAC 246
Qy 241 CCGCTCCGGGATCCCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCCGCCCTTAGAA 300
Db 247 CCGCTCCGGGATCCCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCCGCCCTTAGAA 306
Qy 301 CTTCCCGGTGAGGATCTCCGTCCTCAGCCGCTCACAGCTCTCTCCAGCGCCCATCGCC 360
Db 307 CTTCCCGGTGAGGATCTCCGTCCTCAGCCGCTCACAGCTCTCTCCAGCGCCCATCGCC 366
Qy 361 TTGAGCTGCCACTACCTCTAGACTGCCCTCCCGGCTGGCTGCCAGGAGTCTACGCC 420
Db 367 TTGAGCTGCCACTACCTCTAGACTGCCCTCCCGGCTGGCTGCCAGGAGTCTACGCC 426
Qy 421 GCGGACCCCTTCTCGGGTTACCTCTCTCGGACAGCACCCCTCTCCCTTCTCGGTAGC 480
Db 427 GCGGAC-----CCCTTCTCGGGTAGC 447
Qy 481 TCCTACCCCTGCTGTGCGGCTCTGTCGCCGCCAGCCCTCGGTGCTGCTTCCGACACA 540
Db 448 TCCTACCCCTGCTGTGCGGCTCTGTCGCCGCCAGCCCTCGGTGCTGCTTCCGACACA 507
Qy 541 GCGCGCGCTCTCTCAGCCGCCCTCTGCGCTCGGCCCTCCCTCTCTGCTGCGCCCTGGC 600
Db 508 GCGCGCGCTCTCTCAGCCGCCCTCTGCGCTCGGCCCTCCCTCTCTGCTGCGCCCTGGC 567
Qy 601 GCCATGCGCTGAGCTGAGCTGAGGAGCTGCTGCTGCTCCTGCTGAGCATCTACGAG 660
Db 568 GCCATGCGCTGAGCTGAGCTGAGGAGCTGCTGCTGCTCCTGCTGAGCATCTACGAG 627
Qy 661 GACCCGTGAGCTGAGCTGAGGAGCTGCTGCTGCTCCTGCTGAGCATCTACGAGACTGG 720
Db 628 GACCCGTGAGCTGAGCTGAGGAGCTGCTGCTGCTCCTGCTGAGCATCTACGAGACTGG 687
Qy 721 GTGCGGAGAGGCGCAGGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 688 GTGCGGAGAGGCGCAGGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
Qy 781 CCGCGCTGAGGCGCAGGCTCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 840
Db 748 CCGCGCTGAGGCGCAGGCTCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 807
Qy 841 CTGAGCCCACTCTCAAGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 808 CTGAGCCCACTCTCAAGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
Qy 901 AAGCTCTTCTGCTCAGGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 868 AAGCTCTTCTGCTCAGGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 927
Qy 961 CAGGACGAGCATGAGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTG 1020
Db 928 CAGGACGAGCATGAGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTG 987
Qy 1021 AAGGACCAACTTCAAGCGCGCTTCAAGCAGGCGCGGAAACACACCGAAGCGCTGCACTG 1080
Db 988 AAGGACCAACTTCAAGCGCGCTTCAAGCAGGCGCGGAAACACACCGAAGCGCTGCACTG 1047
Qy 1081 CTGAGGACCAACTGCGGAGACCAAGCTTTCACCAAGAGCTGCGGACCACTATCGGC 1140
Db 1048 CTGAGGACCAACTGCGGAGACCAAGCTTTCACCAAGAGCTGCGGACCACTATCGGC 1107
Qy 1141 GAGGCTTTCAGGCGCTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1108 GAGGCTTTCAGGCGCTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1167
Qy 1201 CTGAGGCGGACACGGCCCGCAGCTGACCACTGACGAGCAAGTCCAGCGCTACAGC 1260
Db 1168 CTGAGGCGGACACGGCCCGCAGCTGACCACTGACGAGCAAGTCCAGCGCTACAGC 1227
Qy 1261 CAGGAGCTGCGGAGCTTCCAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db 1228 CAGGAGCTGCGGAGCTTCCAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1287

Qy 1321 GACCGCACACCTTCTGCTGGCTGGCTGGCTCTCACTGTCCGAGCGGCTCAAGGGAATAATC 1380
Db 1288 GACCGCACACCTTCTGCTGGCTGGCTGGCTCTCACTGTCCGAGCGGCTCAAGGGAATAATC 1347
Qy 1381 CATGAGACCAACCTCACATATGAAGACTTCCCGACCTTCCAAAGTACACAGGCCCTTCGAG 1440
Db 1348 CATGAGACCAACCTCACATATGAAGACTTCCCGACCTTCCAAAGTACACAGGCCCTTCGAG 1407
Qy 1441 TACCACTTGAAGTCCCTGTTCCAGGACATCCACAGTGCAGCGCCCTTAACCTG 1500
Db 1408 TACCACTTGAAGTCCCTGTTCCAGGACATCCACAGTGCAGCGCCCTTAACCTG 1467
Qy 1501 GACCGGCGACAGCCACAGCGCTGATCCTCTGCGACGACTGCACCATTTGTGGCTTAC 1560
Db 1468 GACCGGCGACAGCCACAGCGCTGATCCTCTGCGACGACTGCACCATTTGTGGCTTAC 1527
Qy 1561 GGCAACTTGCACCCACACAGCCACTGCAGACTCGCCAAAGCGCTTCGATGTGGAGGTGCG 1620
Db 1528 GGCAACTTGCACCCACACAGCCACTGCAGACTCGCCAAAGCGCTTCGATGTGGAGGTGCG 1587
Qy 1621 GTGCTGGGTTCTGAAGCTTTCAGTGTGGGCTCCTACTGTGGAGGTGTGTGGCGGAG 1680
Db 1588 GTGCTGGGTTCTGAAGCTTTCAGTGTGGGCTCCTACTGTGGAGGTGTGTGGCGGAG 1647
Qy 1681 AAGACCCAGTGGGTGATCGGGCTGGCACACGACCGCCAAAGCGCGACATCCAG 1740
Db 1648 AAGACCCAGTGGGTGATCGGGCTGGCACACGACCGCCAAAGCGCGACATCCAG 1707
Qy 1741 ATCCAGCCGACCGCGGC 1758
Db 1708 ATCCAGAACCTTGGCTGC 1725

RESULT 12
ID ADC37264 standard; DNA; 2207 BP.
XX ADC37264;
AC ADC37264;
XX
XX 18-DEC-2003 (first entry)
DT
DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 97.
XX
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischaemic disorder; Anti-inflammatory;
KW immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; ds.
XX
OS Homo sapiens.
XX
XX W02003048202-A2.
PN
XX 12-JUN-2003.
XX
XX 03-DEC-2002; 2002WO-JP012644.
PF
XX 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX
XX (ASAH) ASahi Kasei KK.
XX
XX Matsuda A, Muramatsu S;
PI
XX WPI; 2003-505282/47.
DR
XX P-PSDB; ADC37265.
DR
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or

DE Human tumour suppressor CAR-1, BAC clone RP11-150F21 5' sequence.

XX Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
 KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
 KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
 KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
 KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
 KW bacteriella artificial chromosome; chromosome lp31-lp36.

XX Homo sapiens.

XX W0200212285-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US025269.

XX 10-AUG-2000; 2000US-0225033P.

PR 23-AUG-2000; 2000US-0227560P.

XX (TEXA) UNIV TEXAS SYSTEM.

PA Killary A, Chandler D, Lott S;
 XX WPI; 2002-269089/31.

DR New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
 PT diagnosing cancer, for altering the phenotype of a tumor cell, for
 PT treating cancers or as a diagnostic or prognostic indicator of cancer.

XX Disclosure; Page 157-170; 185pp; English.

XX The invention relates to an isolated polynucleotide encoding a
 CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
 CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
 CC from 10-50 amino acids, an expression cassette comprising the
 CC polynucleotide under the control of a promoter operable in eukaryotic
 CC cells, a method for suppressing growth of a cancer cells by contacting
 CC the cells with the expression cassette (i.e. gene therapy), a cell
 CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody, a hybridoma cell that produces the monoclonal
 CC antibody, a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1, or by
 CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC non-transgenic eukaryote, a method of screening a candidate substance for
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
 CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
 CC altering the phenotype of a tumour cell, for treating cancers (e.g.
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
 CC other tissues), and as a diagnostic or prognostic indicator of cancer.
 CC CAR-1 may also be used in screening compounds for activity in either
 CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
 CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
 CC chromosome 1 (lp31-lp36). The present sequence is a BAC (bacterial
 CC artificial chromosome) containing part of the CAR-1 gene

XX Sequence 45845 BP; 12103 A; 10668 C; 10633 G; 12441 T; 0 U; 0 Other;

Query Match	26.0%	Score 995.8;	DB 6;	Length 45845;
Best Local Similarity	99.7%	Pred. No. 2.1e-180;		
Matches 1008;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1;
QY 1	AGGCTGCGCTGGACCGAAGCGGTGGCTTAAAGCTCGCGGGGTAAAGGGTTCGGCTGGG	60		
DB 24164	AGGCTGCGCTGGACCGAAGCGGTGGCTTAAAGCTCGCGGGGTAAAGGGTTCGGCTGGG	24223		
QY 61	CAAGGGTTTGGGGCCGGGATCCGGCAGCTGAGCGGGCCGGCACCCCTCTCTTCTTGCC	120		
DB 24224	CAAGGGTTTGGGGCCGGGATCCGGCAGCTGAGCGGGCCGGCACCCCTCTCTTCTTGCC	24283		
QY 121	GGTACAGCAATGTACGGCTCGGCCTCGCCCTCCCGAGATTCGCCATCCCA	180		
DB 24284	GGTACAGCAATGTACGGCTCGGCCTCGCCCTCCCGAGATTCGCCATCCCA	24343		
QY 181	GCTTCTCGCCCTCCCGCAGCCGCCACCCCGGGATTTCGACCCCTTAAGGGCTCCAC	240		
DB 24344	GCTTCTCGCCCTCCCGCAGCCGCCACCCCGGGATTTCGACCCCTTAAGGGCTCCAC	24403		
QY 241	CCGCTCCGGGATCCCTTCTCCAGCTCTATCCCTTAGAGACTGCGCCCGCCCTAGAA	300		
DB 24404	CCGCTCCGGGATCCCTTCTCCAGCTCTATCCCTTAGAGACTGCGCCCGCCCTAGAA	24463		
QY 301	CCTCCCGCTCAGGATCTCCCTCCCTCAGCCGCTCAGAGCTCTCCCGAGGCCCATCGCC	360		
DB 24464	CCTCCCGCTCAGGATCTCCCTCCCTCAGCCGCTCAGAGCTCTCCCGAGGCCCATCGCC	24523		
QY 361	TTGAGTCCGCCACTACCTCTAGACTGCCCCTCCCGGGCTGGCGTCCCGAGGTCAGCC	420		
DB 24524	TTGAGTCCGCCACTACCTCTAGACTGCCCCTCCCGGGCTGGCGTCCCGAGGTCAGCC	24583		
QY 421	GGCAGCCCTTCTCGGGTTACCTCTTCCGGACAGCACCCCTCTCTCCGGTAGC	480		
DB 24584	GGCAGCCCTTCTCGGGTTACCTCTTCCGGACAGCACCCCTCTCTCCGGTAGC	24643		
QY 481	TCCTACCCCTGCTGTCGGGGCTGCTCCCGCGCCAGCCCTCGGTGCTGCCTCCGACA	540		
DB 24644	TCCTACCCCTGCTGTCGGGGCTGCTCCCGCGCCAGCCCTCGGTGCTGCCTCCGACA	24703		
QY 541	GGCGCGGCTCTCTCAGCCGCCCTTCCCTCGGCCCTTGGGCCCTCTCTGTCGCCCTGGC	600		
DB 24704	GGCGCGGCTCTCTCAGCCGCCCTTCCCTCGGCCCTTGGGCCCTCTCTGTCGCCCTGGC	24762		
QY 601	GCCATGGCGTGCAGCTCAGGAGGAGCTGCTGTGCTCATCTGCTCAGCATATACAG	660		
DB 24763	GCCATGGCGTGCAGCTCAGGAGGAGCTGCTGTGCTCATCTGCTCAGCATATACAG	24822		
QY 661	GACCCGGTGAAGCTGGGCTCGGAGCACTACTTCTGCCCGCGCTGCATCAGGAGCACTGG	720		
DB 24823	GACCCGGTGAAGCTGGGCTCGGAGCACTACTTCTGCCCGCGCTGCATCAGGAGCACTGG	24882		
QY 721	GTGCGGAGAGGCGCAGGCGGCCCGGAGATGCGCCCGAGTGGCGGCGCAGCTTCGCCGAG	780		
DB 24883	GTGCGGAGAGGCGCAGGCGGCCCGGAGATGCGCCCGAGTGGCGGCGCAGCTTCGCCGAG	24942		
QY 781	CCGCGCTGCGGCCCGCCAGCTCAGCTGGCCCAATCGTGAGCGCTACAGCTCTCTCCCG	840		
DB 24943	CCGCGCTGCGGCCCGCCAGCTCAGCTGGCCCAATCGTGAGCGCTACAGCTCTCTCCCG	25002		
QY 841	CTGGAGCCCATCTCAACGCGCGCGCGCGAGCCCTGCCAGGCGCAGCAAGGTC	900		
DB 25003	CTGGAGCCCATCTCAACGCGCGCGCGCGAGCCCTGCCAGGCGCAGCAAGGTC	25062		
QY 901	AAGCTCTTCTGCTCAGGACCGGGCGCTTCTCTGCTTCTTCTGCGAGAGGCTGCACTG	960		
DB 25063	AAGCTCTTCTGCTCAGGACCGGGCGCTTCTCTGCTTCTTCTTCTGCGAGAGGCTGCACTG	25122		
QY 961	CACGAGCAGCATCAGGTCACCGGATCGACGAGCCCTTCCAGCAGGCTGCAG	1011		
DB 25123	CACGAGCAGCATCAGGTCACCGGATCGACGAGCCCTTCCAGCAGGCTGCAG	25173		

```
RESULT 14
ABK12807
ID ABK12807 standard; DNA; 49744 BP.
XX
AC ABK12807;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor CAR-1, BAC clone 392H05 5' sequence.
XX
KW Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteria artificial chromosome; chromosome 1p31-1p36.
XX
OS Homo sapiens.
XX
PN WO200212285-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
PR 10-AUG-2000; 2000US-0225033P.
XX
PR 23-AUG-2000; 2000US-0227560P.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Killary A, Chandler D, Lott S;
XX
PI WPI; 2002-269088/31.
XX
DR
XX
PT New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
PS Disclosure; Page 135-148; 185pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC
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CC CAR-1 may also be used in screening compounds for activity in either stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the effect of mutant CAR-1 molecule. The gene for CAR-1 is located on chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial artificial chromosome) containing part of the CAR-1 gene

Query Match 21.9%; Score 838.6; DB 6; Length 49744;
Best Local Similarity 93.5%; Pred. No. 2.4e-150;
Matches 951; Conservative 0; Mismatches 59; Indels 7; Gaps 7;

QY 1 AGGCTGCGGTGACCGAAGCGGTGGCTGTAGCTCGCGGGGTAGAGGGTCCGCTGGG 60
Db 34306 AGGCTGCGGTGACCGAAGCGGTGGCTGTAGCTCGCGGGGTAGAGGGTCCGCTGGG 34365

QY 61 CCAGGGTTTGGGGCCGGGATCCGGCAGCTGAGCGGCGCGGCACCCCTCTCTCTCTGCC 120
Db 34366 CCA-GGTTTGGGGCCGGGATCCGGCAGCTGAGCGGCGCGGCACCCCTCTCTCTGCC 34424

QY 121 GGTACAGCCAAATGTACGGCTCGGCTGGCTGCCCTCCCGCAGGATTCCTCATCCCCA 180
Db 34425 GGTACAGCCAAATGTACTGCTGGCTGGCTGCCCTCCCGCAGGATTCCTCATCCCCA 34484

QY 181 GCTTCTCGCCCTCCCGCACCGCCCGCCCGGATTTGAGACCCCTTAAAGGGTCCAC 240
Db 34485 GGTCTTGGCCCTTCCCGCACCGCCCGCCCGGATTTGAGACCCCTTAAAGGGTCCAC 34544

QY 241 CCCGCTCCGGGATCCCTTCTCCAGCTCTATTCCTTAGGACTGCCCGCCCTTAGAA 300
Db 34545 CCCGCTCCGGGATCCCTTCTCCAGCTCTATTCCTTAGGACTGCCCGCCCTTAGAA 34604

QY 301 CTCTCCC-GTACAGATCTCCGTC-CTCAGCCGCTCAACA-GCCTCTCCAGCGCCCATC 357
Db 34605 CTCTCCCAGTTAGGATCTCCGTCCTCTCAGCCGCTCATAGCTTCTTTCCAGGCCATT 34664

QY 358 GCG-TTGAGCTGCCACTACC-TCTAGACTGCCCTCCCGGCTGGGCTCCAGGGAGTCT 415
Db 34665 GCGTTTGAGCTGCCCTTACCTTTTATTTGCTTCTCCCGGCTGGCTTTCATGATTTT 34724

QY 416 CAGCGCGCACCCCTTCTCGGTTTACCTTCTCCGAGACAGCCCTTCTCTCCG 475
Db 34725 CAGCGCGCACCCCTTCTCGGTTTACCTTCTCCGAGACAGCCCTTCTCTCCG 34784

QY 476 GTAGTCTTACCCCTGCTGTGCGGGCTGTGTCGCCGCCAGCCCTCGGTGCTGCTC 535
Db 34785 GTAGTCTTACCCAGCTGTGCGGGCTGTGTCGCCGCCAGCCCTCGGTGCTGCTC 34844

QY 536 CGACAGCGCGG-GCTCTCTAGCGCCCTTCTAGCCCTTCTCGGGCCCTCTCTGCTGC 594
Db 34845 CGACAGCGCGGGCTCTATTAGCCGCCCTTCTCGGGCCCTTCTATGCTGCTGC 34904

QY 595 CCTGCGCCATGGCGTGCAGCTCAAGGACGAGCTGTGTGCTCTCCATCTGCTGAGCATC 654
Db 34905 CCTGCGCCATGGCGTGCAGCTCAAGGACGAGCTGTGTGCTCTCCATCTGCTGAGCAT 34964

QY 655 TACAGGACCCGCTGAGCTGTGCGCTGTGCGGCTGTGCTGCTGCTGCTGCTGCTGCT 714
Db 34965 TACAGGACCCGCTGAGCTGTGCGCTGTGCGGCTGTGCTGCTGCTGCTGCTGCTGCT 35024

QY 715 CACTGGGTGCGCAGGAGCGCGCGCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCTGCT 774
Db 35025 CACTGGGTGCGCAGGAGCGCGCGCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCTGCT 35084

QY 775 GCGGAGCCCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCTGCT 834
Db 35085 GCGGAGCCCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCTGCT 35144

QY 835 TTCCCGCTGAGCGCATCTCTAAACGCGCGCGCGCGCGGCTGCGGCTGCGGCTGCGGCTGCTGCT 894
Db 35145 TTCCCGCTGAGCGCATCTCTAAACGCGCGCGCGCGGCTGCGGCTGCGGCTGCGGCTGCTGCT 35204

QY 895 AAGGTCAAGCTTCTGCGCTCAGGACCGCGGCTTCTCTGCTTCTTCTGCGGAGCGCT 954

Db	35205	AAAGTCAAGCTTTTGGCTTCACGACCGGCGCTTCTGCTTCTTTGGACGAGCCT	35264
QY	955	GCACTGCAGCAGCAGCATCAGGTTCACCGCATCGACGAGCCCTTCGACGAGTGCAG	1011
Db	35265	GCACTGCAGCAGCAGCATCAGGTTCACCGCATTCGACGAGCCTTCGACGAGTGCAG	35321
RESULT 15			
ID	AAH06784	standard; cDNA; 628 BP.	
XX	AAH06784;		
AC	AAH06784;		
XX	26-JUN-2001	(first entry)	
DT	Human cDNA clone (5'-primer)	SEQ ID NO:3619.	
DE	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.		
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.		
KW	Homo sapiens.		
OS	EP1074617-A2.		
XX	07-FEB-2001.		
PD	28-JUL-2000; 2000EP-00116126.		
XX	29-JUL-1999; 99JP-00248036.		
PR	27-AUG-1999; 99JP-00300253.		
PR	11-JAN-2000; 2000JP-00118776.		
PR	02-MAY-2000; 2000JP-00183767.		
PR	09-JUN-2000; 2000JP-00241899.		
XX	(HELI-) HELIX RES INST.		
PA	Ora T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
XX	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
PI	WPI; 2001-318749/34.		
XX	Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.		
PT	Claim 1; SEQ ID NO 3619; 2537pp + Sequence Listing; English.		
PS	The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any special methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention		
XX	Sequence 628 BP; 83 A; 269 C; 170 G; 103 T; 0 U; 3 Other;		

Query Match	15.5%;	Score 592.2;	DB 4;	Length 628;
Best Local Similarity	97.3%;	Pred. No. 1.3e-103;		
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Gaps	1;			
QY	370	CCACTACCTTCTAGACTGCGGCTCCGGGCTGGCGTCCACGGAGTCTCAGCGCGCACCCC	429	
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QY	430	TTCTCTGGCGTTTACCTTCCCTCCGGACAGACACCCCTCTCTCCGCTAGCTCTCTACCCC	489	
Db	61	TTCTCTGGCGTTTACCTTCCCTCCGGACAGACACCCCTCTCTCCGCTAGCTCTCTACCCC	120	
QY	490	TGCTCTGGCGGCTCTGCTCCCGCGCCAGCCCTCGGTCTGCTCGACAGCGCCGCGC	549	
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QY	550	TCTCTCAGCGCGCCCTCTGCGGCTCCCGCTCTCTCTGCTGCGCTTGGCGGCTGGCG	609	
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Db	301	AGCTTGGGCTGCGAGCACTACTTTCGCCGCGCTGTCATCAGGAGCACTGGGTGCGGAG	360	
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QY	790	GCGCCAGCTCAAGCTGGGCAACATCTGCGGCTGAGCTCTCTTCCGCTGCGAGCC	849	
Db	421	GCGCCAGCTCAAGCTGGGCAACATCTGCGGCTGAGCTCTCTTCCGCTGCGAGCC	480	
QY	850	ATCTCTAACGCGCGCGCGCGGCTGCGGCTGCGGCGGCGGCTGCGGCGGCGGCTG	909	
Db	481	ATCTCTAACGCGCGCGCGCGGCTGCGGCTGCGGCGGCGGCTGCGGCGGCGGCTG	540	
QY	910	TGCTCTACGAGCGCGCGGCTTCTGCTTCTTCTGCGAGC-AGCTGCTGCTGCGAGCA	968	
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Search completed: July 31, 2004, 12:54:57
Job time : 1378 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 16:55:22 ; Search time 1585 Seconds
(without alignments)
11835.592 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggtcgctgacggaagc.....aaaaaaaaaaaaaaaaaaaa 3826

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2322.2	60.7	23433	9	US-09-927-091-7
3	2308.6	60.3	30676	9	US-09-927-091-8
4	2252.8	58.9	30625	9	US-09-927-091-5
5	995.8	26.0	45845	9	US-09-927-091-6
6	838.6	21.9	49744	9	US-09-927-091-4
7	609.6	15.9	610	13	US-10-027-632-100265
8	609.6	15.9	610	16	US-10-027-632-100265
9	562	14.7	573	9	US-09-864-761-7231
10	431	11.3	431	9	US-09-864-761-23962
11	160.2	4.2	2045	16	US-10-094-749-1459
12	136.4	3.6	1394	9	US-09-764-868-418
13	132.4	3.5	3038	16	US-10-120-988-277
14	122.8	3.2	1904	16	US-10-104-047-103

15	122	3.2	1739	9	US-09-731-872-225	Sequence 225, App
16	122	3.2	1739	10	US-09-876-997-225	Sequence 225, App
17	122	3.2	12733	15	US-10-032-393-47	Sequence 47, Appli
18	122	3.2	12739	15	US-10-032-393-8	Sequence 8, Appli
19	119.2	3.1	3479	13	US-10-147-493-123	Sequence 123, App
20	119.2	3.1	3479	13	US-10-145-127-123	Sequence 123, App
21	119.2	3.1	3479	13	US-10-160-503-123	Sequence 123, App
22	119.2	3.1	3479	13	US-10-143-118-123	Sequence 123, App
23	119.2	3.1	3479	13	US-10-144-993-123	Sequence 123, App
24	119.2	3.1	3479	13	US-10-158-787-123	Sequence 123, App
25	119.2	3.1	3479	13	US-10-140-024-123	Sequence 123, App
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28	119.2	3.1	3479	13	US-10-127-852A-123	Sequence 123, App
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36	119.2	3.1	3479	13	US-10-157-798-123	Sequence 123, App
37	119.2	3.1	3479	15	US-10-028-072-123	Sequence 123, App
38	119.2	3.1	3479	15	US-10-121-049-123	Sequence 123, App
39	119.2	3.1	3479	15	US-10-123-904-123	Sequence 123, App
40	119.2	3.1	3479	15	US-10-140-470-123	Sequence 123, App
41	119.2	3.1	3479	15	US-10-175-746-123	Sequence 123, App
42	119.2	3.1	3479	15	US-10-176-918-123	Sequence 123, App
43	119.2	3.1	3479	15	US-10-176-921-123	Sequence 123, App
44	119.2	3.1	3479	15	US-10-137-865-123	Sequence 123, App
45	119.2	3.1	3479	15	US-10-140-474-123	Sequence 123, App

ALIGNMENTS

RESULT 1
US-09-927-091-3
; Sequence 3, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3826
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-3

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								0;
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Db	1	AGGCTCGCTGGACCGAAGCGGTGGCTAGCTCGCGGGGTAAAGGGTCCGCTGGG	60					
QY	61	CCAGGGTTTGGGGCCCGGATCCCGAGCTAGCGGGCCCGGACCCCTCTCTCTGCC	120					
Db	61	CCAGGGTTTGGGGCCCGGATCCCGAGCTAGCGGGCCCGGACCCCTCTCTCTGCC	120					
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RESULT 3			
US-09-927-091-8			
; Sequence 8, Application US/09927091			
; Patent No. US20020119541A1			
; GENERAL INFORMATION:			
; APPLICANT: KILLARY, ANN			
; APPLICANT: LOTT, STEVE			
; APPLICANT: CHANDLER, DAWN			
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1			
; FILE REFERENCE: UTSC:651US			
; CURRENT APPLICATION NUMBER: US/09/927,091			
; CURRENT FILING DATE: 2001-08-09			
; PRIOR APPLICATION NUMBER: 60/227,560			
; PRIOR FILING DATE: 2000-08-23			
; PRIOR APPLICATION NUMBER: 60/225,033			
; PRIOR FILING DATE: 2000-08-10			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 8			
; LENGTH: 30676			
; TYPE: DNA			
; ORGANISM: Human			
; FEATURE:			
; NAME/KEY: modified base			
; LOCATION: (6671)..(30676)			
; OTHER INFORMATION: n = A or C or G or T/U			
US-09-927-091-8			
Query Match 60.3%; Score 2308.6; DB 9; Length 30676;			
Best Local Similarity 98.7%; Pred. No. 0;			
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QY	1489	GCCTAACCTTGGACCCGGGCACAGCCACAGCGCTGATCTCTGTCGGAGCATGCAAC	1548
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QY 3589 CAACACACATCCCAAGTAGCGGAGAGCTAAACACAGGGGGTCTTAAATGGCTGC 3648
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Db 25649 CTACAGATCTGGGCCACCCAGAGTATTTTATTTAAATGTTGCCATTTATGAG 25708
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Db 25709 TTATGATCAATTTGTTAAATTAAGTTACAGATGTCA 25747

RESULT 4

US-09-927-091-5
; Sequence 5, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 30625
; TYPE: DNA
; ORGANISM: Human
; FEATURE:

; NAME/KEY: modified base
; LOCATION: (4754)..(30625)
; OTHER INFORMATION: n = A or C or G or T/U
US-09-927-091-5
Query Match 58.9%; Score 2252.8; DB 9; Length 30625;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 57; Indels 3; Gaps 3;
QY 1429 GGGCCCCCTGAGTACACATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCAGCC 1488
Db 21906 GGTCCACACCCCTTCTCCCACTCATCTCTCTCTCCCTCTCCACCCCCACAGTGCAGCC 21965
QY 1489 GCCCTAAACCCCTGGACCCGGGACAGCCACCCAGAGCCCTGATCTCTGTCCGACGACTGCACC 1548
Db 21966 GCCCTAAACCCCTGGACCCGGGACAGCCACCCAGAGCCCTGATCTCTGTCCGACGACTGCACC 22025
QY 1549 ATTGTGGCTTACGGCAATCTGCACCCACAGCCACTGAGGACTGCCAAAGGCTTCAT 1608
Db 22026 ATTGTGGCTTACGGCAATCTGCACCCACAGCCACTGAGGACTGCCAAAGGCTTCAT 22085
QY 1609 GTGGAGGTGTCGGTCTGGGTTCTGAAGCCTTTCAGTAGTGGCTCCACTACTTGGGAGGTG 1668
Db 22086 GTGGAGGTGTCGGTCTGGGTTCTGAAGCCTTTCAGTAGTGGCTCCACTACTTGGGAGGTG 22145
QY 1669 GTGTGGCGGAGAAAGACCCAGTGGGTGATCGGGCTGGCACAGAAAGCCGCAAG 1728
Db 22146 GTGTGGCGGAGAAAGACCCAGTGGGTGATCGGGCTGGCACAGAAAGCCGCAAG 22205
QY 1729 GGCAGATCCAGATCCAGCCAGCCGCGGCTTCTACTGATCGTGTGATGACGATGGCAC 1788
Db 22206 GGCAGATCCAGATCCAGCCAGCCGCGGCTTCTACTGATCGTGTGATGACGATGGCAC 22265
QY 1789 CAGTACAGGCTGACAGCCAGCCCTGGACGGGCTTAAAGTCCGGGACAAAGCTTGACAAAG 1848
Db 22266 CAGTACAGGCTGACAGCCAGCCCTGGACGGGCTTAAAGTCCGGGACAAAGCTTGACAAAG 22325
QY 1849 GTGGGTGCTTCTCTCGACTATGACCAAGGCTTGCTCATCTTCTCAATGCTGATGACATG 1908
Db 22326 GTGGGTGCTTCTCTCGACTATGACCAAGGCTTGCTCATCTTCTCAATGCTGATGACATG 22385
QY 1909 TCTTGGCTTACACCTTCCGAGAAAGTTCCTTGGCAAGCTTGCTTCTTACTTTCAGCCCT 1968
Db 22386 TCTTGGCTTACACCTTCCGAGAAAGTTCCTTGGCAAGTTCCTTGGCAAGCTTGCTTCTTACTT 22445
QY 1969 GGCAGAGCCAGCCCAATGGCAAGAGCTTTCAGCCGCTCGGATCAACACCCGTCGCCATC 2028
Db 22446 GGCAGAGCCAGCCCAATGGCAAGAGCTTTCAGCCGCTCGGATCAACACCCGTCGCCATC 22505
QY 2029 TAGTCCAGCAGAGGAGACCAACCTCTCTGGGACCACTGCGACCTGCAAGAGCCCTGC 2088
Db 22506 TAGTCCAGCAGAGGAGAAACAA-CTCCTGGAAACACTGCCACCTGCAAGAGCCCTGC 22564
QY 2089 CCAGGAGATAGAACCTTGGATCCAGCCCAAGCTGGCCACTTGGAGACTCAGGCCACT 2148
Db 22565 CCAGG-AGATAGAAACCTTGGATCCAGCCCAAGCTGGCCACTTGGAGACTCAGGCCACT 22623
QY 2149 TGTTTACCTCCAGCCCTCAGTCTGTAAATGAGGTTGCAITTCCTTCTTCTTAAATC 2208
Db 22624 TGTTTACCTCCAGCCCTCAGTCTGTAAATGAGGTTGCAITTCCTTCTTCTTAAATC 22683
QY 2209 TCTTCCAGCATCGATGTTCTGATGCTCTGACCTTGTATGAGGATAGAGCTTGTATCCAGG 2268
Db 22684 TCTTCCAGCATCGATGTTCTGATGCTCTGACCTTGTATGAGGAAACAGCTTGTATCCAAAG 22743
QY 2269 ATGTGATGCTGCTTCTCTCAGGCAACCCCTGCCCAACCTCATCCCCATCTTCTCAGG 2328
Db 22744 ATGTGATGCTGCTTCTCTCAGGCAACCCCTGCCCAACCTCATCCCCATCTTCTCAGG 22803
QY 2329 GGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAAGTGTGAG 2388
Db 22804 GGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAAGTGTGAG 22863

QY	2389	AGCATGCCAGTAGTTGGCAGCCGGAAGACACACAGCACCCCTTTATGTCTATGTCCCATGGCCT	2448
DB	22864	AGCATGCCAGTAGTTGGCAGCCGGAAGACACACAGCACCCCTTTATGTCTATGTCCCATGGCCT	22923
QY	2449	AAGACTTACCCCTGACCAACAGCTAGTCATGGCCATTATCCCTTGACCCCAAGTCCACAGTG	2508
DB	22824	AAGACTTACCCCTGACCAACAGCTAGTCATGGCCCAITATCCCTTGACCCCAAGTCCACAGTG	22983
QY	2509	GTACAGGTAGTACCTGGTCTTAGGGTTGGCTCAGAGGCCAAACCTCTCTCCGCCACCCCCAC	2568
DB	22984	GTACAGGTAGTACCTGGTCTTAGGGTTGGCTGAAAGCCAAACCTCTCTCCGCCACCCCCAC	23043
QY	2569	ACCAAGAACTATATGGTCTCTATCTTCCCACTGATCTGTGTGTGATGATGATGATG	2628
DB	23044	ACCAAGAAATATATGGTCTCTATCTTCCCACTGATCTGTGTGTGATGATGATGATG	23103
QY	2629	GCCTGTGGAAGGCACCTGGTGTAGTGTGACACATATAGTCAATGTGACACACCTTCC	2688
DB	23104	GCCTGTGGAAGGCACCTGGTAAITGTAATCCACATATATAGTCAATGTGACACACCTTCC	23163
QY	2689	TGCCACAGGCCGAGGACAGGGTGAAGGTATACCCAAAGCTGATGCAGAGCCCAATTAGC	2748
DB	23164	TGCCACAGGCCGAGGACAGGGTGAAGGTATACCCAAAGCTGATGCAGAGCCCAATTAGC	23223
QY	2749	CTAAAGCAACTGCAGACAAGGCTCCCTGGATGATCGAGGTCCCCAGTAGCTCTGAACA	2808
DB	23224	CTAAAGCAACTGCAGACAAGGCTCCCTGGATGATCGAGGTCCCCAGTAGCTCTGAACA	23283
QY	2809	AGAGTCAGACCAACCTCTTCAGCCAGGCTCTGTGACCTGTAGGCTGAGGAGGCTTC	2868
DB	23284	AGAGTCAGACCAACCTCTTCAGCCAGGCTCTGTGACCTGTAGGCTGAGGAGGCTTC	23343
QY	2869	CAGAAGCAGTTGTTGTAATTAGGACCCAAAGCACT--GGGAGGGGCTGTTGGCTAGACCCCT	2927
DB	23344	CAGAAGCAGTTGTTGTAATTAGGACCCAAAGCACTGGGAGGGGCTGTTGGCTAATACCCCT	23403
QY	2928	TGTCAGACTGGCACTCTATCTCAGTTAGGATCTGCTGCAGAAAAACAAGAGCCACTTGTA	2987
DB	23404	TGTCAGACTGGCACTCTATCTCAGTTAGGATCTGCTGCAGAAAAACAAGAGCCACTTGTA	23463
QY	2988	GCCTGTTTAATTAGACAAGGATTTACTACTGGCCCTGTGGCTTGCAAAATGTTGGGA	3047
DB	23464	GCCTGTTTAATTAGACAAGGATTTACTACTGGCCCTGTGGCTTGCAAAATGTTGGGA	23523
QY	3048	AGAGCTGGGAAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGCGCCAGATTCTCATGT	3107
DB	23524	AGAGCTGGGAAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGCGCCAGATTCTCATGT	23583
QY	3108	CTGTGTTGTGCACGAAAGAGTGTGCCCACTGTGGAAGGCCACTATGCGCAAGAAAGTCT	3167
DB	23584	CTGTGTTGTGCACGAAAGAGTGTGCCCACTGTGGAAGGCCACTATGCGCAAGAAAGTCT	23643
QY	3168	GACTGCAGAACTAGGCTCCCTCTGCCAGGTCGGTGCAGCCCAATAGATGTCTGAGGCC	3227
DB	23644	GACTGCAGAACTAGGCTCCCTCTGCCAGGTCGGTGCAGCCCAATAGATGTCTGAGGCC	23703
QY	3228	TGCCCTCTCCCACTTCACTCAGTTCGCCAAATCTAAATTTTACAAGAGATTCTGTTGG	3287
DB	23704	TGCCCTCTCCCACTTCACTCAGTTCGCCAAATCTAAATTTTACAAGAGATTCTGTTGG	23763
QY	3288	GGAACTTAAGTCAGATCCAGAACCTTGGCTCAGAGGAGTCTGGGAAATGTCAATTCCC	3347
DB	23764	GGAACTTAAGTCAGATCCAGAACCTTGGCTCAGAGGAGTCTGGGAAATGTCAATTCCC	23823
QY	3348	TAGAAGGAAGTTAGGTTGGTGGAGCAAGCCCCCACTGGTTTTTCTGCCACAGCATCCA	3407
DB	23824	TAGAAGGAAGTTAGGTTGGTGGAGCAAGCCCCCACTGGTTTTTCTGCCACAGCATCCA	23883
QY	3408	ATCGTCAAGAAACTCGGGAAGGGTGGAGTCCACATCTAGGGTTGTCTGCCCTTGGCTC	3467
DB	23884	ATCGTCAAGAAACTCGGGAAGGGTGGAGTCCACATCTAGGGTTGTCTGCCCTTGGCTC	23943
QY	3468	TATCTCTGCCAGAGTGGAACTCGAGAGAGTGGGCTCGAAGACTGAGCCCTAAATGTCTC	3527

Db	23944	TATCCCTGCCAGAGTGGGAACTGGAGAGTGGCTGC AAAACTGAGCTAAATGTCTC	24003
Qy	3528	CCGGCCCTTGCATTTCTTTCTAGTCTGGGGCTAGATTCTGCACTTGGGGTCTCTGAC	3587
Db	24004	CCGGCCCTTGCATTTCTTTCTAGTCTGGGGCTAAATTTCTGCACTTGGGGTCTCTGAC	24063
Qy	3588	ACAACACACCATCCCAAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTTAAATGGCTG	3647
Db	24064	ACAACACACCATCCCAAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTTAAATGGCTG	24123
Qy	3648	CCCCGCCACCCCGGGCTCCCTTTGGGCAAAAGGAATTGTGAGCCCTACCCCAACCCCTTCA	3707
Db	24124	CCCCGCCACCCCGGGCTCCCTTTGGGCAAAAGGAATTGTGAGCCCTACCCCAACCCCTTCA	24183
Qy	3708	ACTACAGAAATCTGGGCGACCCAGCAGTATTTTATTTAAATGTGCCCATTTTATGA	3767
Db	24184	ACTACAGAAATCTGGGCGACCCAGCAGTATTTTATTTAAATGTGCCCATTTTATGA	24243
Qy	3768	GTTATGATCAATTTGTATTAAATTAAAGTTACAGATGTCA	3807
Db	24244	GTTATGATCAATTTGTATTAAATTAAAGTTACAGATGTCA	24283
RESULT 5			
US-09-927-091-6			
; Sequence 6, Application US/09927091			
; Patent No. US20020119541A1			
; GENERAL INFORMATION:			
; APPLICANT: KILLARY, ANN			
; APPLICANT: LOTT, STEVE			
; APPLICANT: CHANDLER, DAWN			
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1			
; FILE REFERENCE: UTSC:651US			
; CURRENT APPLICATION NUMBER: US/09/927,091			
; CURRENT FILING DATE: 2001-08-09			
; PRIOR APPLICATION NUMBER: 60/227,560			
; PRIOR FILING DATE: 2000-08-23			
; PRIOR APPLICATION NUMBER: 60/225,033			
; PRIOR FILING DATE: 2000-08-10			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 6			
; LENGTH: 45845			
; TYPE: DNA			
; ORGANISM: Human			
US-09-927-091-6			
Query Match 26.0%; Score 995.8; DB 9; Length 45845;			
Best Local Similarity 99.7%; Pred. No. 4.2e-267;			
Matches 1008; Conservative 0; Mismatches 2; Indels 1; Gaps 1;			
Qy	1	AGGCTCGCTGGACCGAAGCGGTGCTGCTAAGCTCGCGGGGGTAAGGGGTGCGGCTGGG	60
Db	24164	AGGCTCGCTGGACCGAAGCGGTGCTGCTAAGCTCGCGGGGGTAAGGGGTGCGGCTGGG	24223
Qy	61	CGAGGGTTTGGGCGCGGGATCCGGCAGCTGAGCGGGCCGGACCCCTCTCTCTCTGCC	120
Db	24224	CGAGGGTTTGGGCGCGGGATCCGGCAGCTGAGCGGGCCGGACCCCTCTCTCTCTGCC	24283
Qy	121	GGTCACAGCCAATGTACGGCTCGGCTCGGCTGCCCTCCCTCCCGCAGGATTCGCCATCCCCA	180
Db	24284	GGTCACAGCCAATGTACGGCTCGGCTCGGCTGCCCTCCCTCCCGCAGGATTCGCCATCCCCA	24343
Qy	181	GCTTCTGCGCCTCCCGCAACCGCCCGCCACCCCGGGATTTCGACCCCTTAAAGGGCTCCAC	240
Db	24344	GCTTCTGCGCCTCCCGCAACCGCCCGCCACCCCGGGATTTCGACCCCTTAAAGGGCTCCAC	24403
Qy	241	CCGCTCCGGGATCCCGCTTCTCCAGCTGCTTATCCCTTAGAGCTGCGCCGCCCTAGAA	300
Db	24404	CCGCTCCGGGATCCCGCTTCTCCAGCTGCTTATCCCTTAGAGCTGCGCCGCCCTAGAA	24463
Qy	301	CCTCCCGGTACAGGATCTCCGTCCTCTCAGCGCTCACAAGCCCTCTCCAGCGCCCTATCGCT	350

Db 24464 CCTCCCGCTCAGGATCTCCGTCCTCAGCGCTCAGAGCTCTCTCCAGCGCCATCGCC 24523
Qy 361 TTGAGCTGCCACTACCTCTAGACTGCGCTCCCGGCTGGGCTCCACGGAGTCTACGCC 420
Db 24524 TTGAGCTGCCACTACCTCTAGACTGCGCTCCCGGCTGGGCTCCACGGAGTCTACGCC 24583
Qy 421 GCGCACCCCTTCCTCGGCTTACCTCTCTTCGGGACAGACCCCTCTCCGTTCTCGGTAGC 480
Db 24584 GCGCACCCCTTCCTCGGCTTACCTCTCTTCGGGACAGACCCCTCTCCGTTCTCGGTAGC 24643
Qy 481 TCCTACCCCTGCTGCTGGGCTCTGCTCCCGGCTGGGCTCTGCTCTGCTCTGCTCTGCT 540
Db 24644 TCCTACCCCTGCTGCTGGGCTCTGCTCCCGGCTGGGCTCTGCTCTGCTCTGCTCTGCT 24703
Qy 541 GCGCGGCTCTCTCAGCGGCTCCCTCTGCGGCTCCCGGCTCTGCTCTGCTCTGCTCTGCT 600
Db 24704 GCGCGGCTCTCTCAGCGGCTCCCTCTGCGGCTCCCGGCTCTGCTCTGCTCTGCTCTGCT 24762
Qy 601 GCCATGGGCTGAGCTCAAGGACGAGTCTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 660
Db 24763 GCCATGGGCTGAGCTCAAGGACGAGTCTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 24822
Qy 661 GACCGGCTGAGCTGAGGCTGAGCACTTCTGCGGCTGAGTCTGCTCTGCTCTGCTCTGCT 720
Db 24823 GACCGGCTGAGCTGAGGCTGAGCACTTCTGCGGCTGAGTCTGCTCTGCTCTGCTCTGCT 24882
Qy 721 GTGCGGAGGAGGCGGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAG 780
Db 24883 GTGCGGAGGAGGCGGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAG 24942
Qy 781 CCGGCTGAGGCGGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCT 840
Db 24943 CCGGCTGAGGCGGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCT 25002
Qy 841 CTGAGCGCATCTCTCAAGCGGCGGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCT 900
Db 25003 CTGAGCGCATCTCTCAAGCGGCGGCGGCTGAGTCTGCGGCTGAGTCTGCGGCTGAGTCT 25062
Qy 901 AAGCTCTTCTGCTCAGGAGCGGCGGCTTCTCTGCTCTTCTGCGAGGCTGCACTG 960
Db 25063 AAGCTCTTCTGCTCAGGAGCGGCGGCTTCTCTGCTCTTCTGCGAGGCTGCACTG 25122
Qy 961 CACGAGCAGATCAGGTACCGGATCAGAGCGCTTCTGAGGCTGAG 1011
Db 25123 CACGAGCAGATCAGGTACCGGATCAGAGCGCTTCTGAGGCTGAG 25173

RESULT 6

US-09-927-091-4
; Sequence 4, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 49744
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-4

Query Match

21.9%; Score 838.6; DB 9; Length 49744;

Best Local Similarity 93.5%; Pred. No. 5.1e-223;
Matches 951; Conservative 0; Mismatches 59; Indels 7; Gaps 7;
Qy 1 AGGCTGCGCTGAGACCGGAGCGGTGGCTGCTAAGCTCGGGGGGTAAAGGGTTCGGCTGGG 60
Db 34306 AGGCTGCGCTGAGACCGGAGCGGTGGCTGCTAAGCTCGGGGGGTAAAGGGTTCGGCTGGG 34365
Qy 61 CCAGGGTTTGGGCGCGGATCCCGACGCTGAGCGGGCGGCAACCCCTCTCTTCTCTGCTCC 120
Db 34366 CCA-GGTTTGGGCGCGGATCCCGACGCTGAAACGGGCGGCAACCCCTCTCTTCTCTGCTCC 34424
Qy 121 GGTACACGCAATGATAGGGTTCGGCTGCGCTCCCTCCCGAGGATTCGCCATCCCA 180
Db 34425 GGTACACGCAATGATAGGGTTCGGCTGCGCTCCCTCCCGAGGATTCGCCATCCCA 34484
Qy 181 GCTTCTGCGCTTCCCGGACCGGCGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 240
Db 34485 GCTTCTGCGCTTCCCGGACCGGCGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 34544
Qy 241 CCGCTCGGGATCCCTTCTCCAGCTCTCTATCCCTTAGGACTGCGCGGCGGCTCTAGAA 300
Db 34545 CCGCTCGGGATCCCTTCTCCAGCTCTCTATCCCTTAGGACTGCGCGGCGGCTCTAGAA 34604
Qy 301 CCTCCCC-GTCAGGATCTCGCTC-CCTCAGCGCTCACA-GCCTCTCTCCAGCGGCTCATC 357
Db 34605 CCTCCCCAGTTAGGATCTCGCTCCTCAGCGCTCATCAGCTTCTTTCAGCGGCTCATC 34664
Qy 358 GCC-TTGAAGTGGCCACTACC-TCTAGACTGCTCTCCGCTCGGCTGGCTGGCTGGCTGGCT 415
Db 34665 GCCTTGAAGTGGCCACTACC-TCTAGACTGCTCTCCGCTCGGCTGGCTGGCTGGCTGGCT 34724
Qy 416 CAGCGGCGACCCCTTCTCGCTGCTTACCTCTCTTCCGACAGACACCCCTCTCTCTCTCCG 475
Db 34725 CAGCGGCGACCCCTTCTCGCTGCTTACCTCTCTTCCGACAGACACCCCTCTCTCTCTCCG 34784
Qy 476 GTAGTCTCTACCTCTGCTGCGGCTCTGCTGCGGCTCTGCTGCGGCTCTGCTGCGGCTCT 535
Db 34785 GTAGTCTCTACCTCTGCTGCGGCTCTGCTGCGGCTCTGCTGCGGCTCTGCTGCGGCTCT 34844
Qy 536 CGACGAGCGCG-GCTCTCTCAGCGGCGGCTCTGCTGCGGCTCTGCTGCGGCTCTCTGCTGCT 594
Db 34845 CGACGAGCGCGGCTCTTATAGCGGCGGCTCTGCTGCGGCTCTGCTGCGGCTCTTATGCTGCT 34904
Qy 595 CCTGCGCATGCGGTGAGCTCAAGGACGAGTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 654
Db 34905 CTTGCGCATGCGGTGAGCTCAAGGACGAGTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 34964
Qy 655 TACCAGGACCGGTGAGCTGCGGCTGCGAGCACTAATTCTGCGGCTGCTGCTGCTGCTGCTGCT 714
Db 34965 TACCAGGACCGGTGAGCTGCGGCTGCGAGCACTAATTCTGCGGCTGCTGCTGCTGCTGCTGCT 35024
Qy 715 CACTGGGTGCGGAGGAGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 774
Db 35025 CACTGGGTGCGGAGGAGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 35084
Qy 775 GCCGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 834
Db 35085 GCCGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 35144
Qy 835 TTCCCGCTGGAAGCCATCTCTCAACCGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 894
Db 35145 TTCCCGCTGGAAGCCATCTCTCAACCGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 35204
Qy 895 AAGGTCAAGCTTCTCTGCTCAGGACCGGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCT 954
Db 35205 AAGGTCAAGCTTCTCTGCTCAGGACCGGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCT 35264
Qy 955 GCATGTCAGGACGATCAGGTACCGGATTCAGGACGCTTTCAGAGGCTGAG 1011
Db 35265 GCATGTCAGGACGATCAGGTACCGGATTCAGGACGCTTTCAGAGGCTGAG 35321

RESULT 7


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US-10-027-632-100265/c
; Sequence 100265, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100265
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-100265

Query Match      15.9%;   Score 609.6;   DB 13;   Length 610;
Best Local Similarity 99.8%;   Pred. No. 6.9e-160;
Matches 609;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY      2345  CCAGTGTCCTCCTCCAGCCCGCCCTGACCTCAGGAAGTGTCAGAGATGCGCCAGTAGTT 2404
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QY      2405  GGCAAGCCGAAAGACACACAGCACCCCTCTATGTCCTCCAGTCCCTTAAGACTTAACCCCTGAC 2464
Db      550  GGCAAGCCGAAAGACACACAGCACCCCTCTATGTCCTCCAGTCCCTTAAGACTTAACCCCTGAC 491
QY      2465  CAAGCTAGTGATGGGCCATTATACCCCTTGACCCCAAGTCCACAGTGGTCACAGGTAGTACCT 2524
Db      490  CAAGCTAGTGATGGGCCATTATACCCCTTGACCCCAAGTCCACAGTGGTCACAGGTAGTACCT 431
QY      2525  GGTCTAGGTTGGCTGAGAGCCAACTCTCTGTCGCCACCCCAACCAAGAACTATATGG 2584
Db      430  GGTCTAGGTTGGCTGAGAGCCAACTCTCTGTCGCCACCCCAACCAAGAACTATATGG 371
QY      2585  TTCTACTTCTCCACATGATCTGTGGTCAAGTATGTCGTGCTGAGTATGTCGTGGCTGTGGAAGCACC 2644
Db      370  TTCTACTTCTCCACATGATCTGTGGTCAAGTATGTCGTGCTGAGTATGTCGTGGCTGTGGAAGCACC 311
QY      2645  TGTTAGTTAGTCCACACATTATAGTGCACCCACCTTCTGTCGCCACAGGCGGAGG 2704
Db      310  TGTTAGTTAGTCCACACATTATAGTGCACCCACCTTCTGTCGCCACAGGCGGAGG 251
QY      2705  GACAGGTTAGGGTATACCCAAAGCTGATGCAGAGCCCAATTAGCTTAAAGCAACTGCAG 2764
Db      250  GACAGGTTAGGGTATACCCAAAGCTGATGCAGAGCCCAATTAGCTTAAAGCAACTGCAG 191
QY      2765  GACAAGCCTCCCTGGATGATCGAGGTCCCAGTAGTCTCTGAAACAAGTCCAGCCAAACC 2824
Db      190  GACAAGCCTCCCTGGATGATCGAGGTCCCAGTAGTCTCTGAAACAAGTCCAGCCAAACC 131
QY      2825  TCTTCAGCCAGGCTCTGTGACCTGCTAGGGTGCAGAGGCTTCCAGAGCAAGTCTGTTGT 2884
Db      130  TCTTCAGCCAGGCTCTGTGACCTGCTAGGGTGCAGAGGCTTCCAGAGCAAGTCTGTTGT 71
QY      2885  AATTAGGACCCAAAGCACTGGAGGGGCTGTGGCTAGACCCCTTGTCAAGCTTGGCATCT 2944

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QY 2765 GACAAAGCTCCCTGGATGATCGAGGTCCCAAGTAGCTCTGAACAAGAGTCCAGCAACCC 2824
Db 190 GACAAGCTCCCTGGATGATCGAGGTCCCAAGTAGCTCTGAACAAGAGTCCAGCAACCC 131
QY 2825 TCTTCAGCAGGCTCTGTGACCTGCTAGGTCAGGAGCTTCCAGAAGCAGTTGTTGT 2884
Db 130 TCTTCAGCAGGCTCTGTGACCTGCTAGGTCAGGAGCTTCCAGAAGCAGTTGTTGT 71
QY 2885 AATTAGGACCAAGCACTCGGAGGGGCTGTTGGCTAGACCCCTTGTCCAGACTTGGCACT 2944
Db 70 AATTAGGACCAAGCACTCGGAGGGGCTGTTGGCTAGACCCCTTGTCCAGACTTGGCACT 11
QY 2945 ATCTCAGTTA 2954
Db 10 ATCTCAGTTA 1

RESULT 9
US-09-864-761-7231/c
; Sequence 7231, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 7231
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; OTHER INFORMATION: MAP TO AC022262.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
; US-09-864-761-7231
Query Match 14.7%; Score 562; DB 9; Length 573;
Best Local Similarity 99.8%; Pred. No. 1.5e-146;
Matches 573; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1602 CTTTCGATGTGGAGGTGTCGGTTCCTGAGCCCTTCAGTAGTCGCGTCCACTACTG 1661
Db 573 CTTTCGATGTGGAGGTGTCGGTTCCTGAGCCCTTCAGTAGTCGCGTCCACTACTG 514
QY 1662 GGAGGTGCTGTCGGCGGAGAGACCCAGTGGGTGATCGGGCTGGCACACGAGCCGCAAG 1721
Db 513 GGAGGTGCTGTCGGCGGAGAGACCCAGTGGGTGATCGGGCTGGCACACGAGCCGCAAG 454
QY 1722 CCGCAAGGGCAGCATCCAGATCCAGCCAGCCGGGCTTCTACTGTCATCGTGCCAGA 1781
Db 453 CCGCAAGGGCAGCATCCAGATCCAGCCAGCCGGGCTTCTACTGTCATCGTGCCAGA 394
QY 1782 TGGCAACCAAGTACAGCCCTTCAGCGAGCCCTGAGCGGCTTAACGTCCTGGGCAAGCT 1841
Db 393 TGGCAACCAAGTACAGCCCTTCAGCGAGCCCTGAGCGGCTTAACGTCCTGGGCAAGCT 334
QY 1842 TGACAAGGTGGTGTCTTCTCTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGA 1901
Db 333 TGACAAGGTGGTGTCTTCTCTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGA 274
QY 1902 TGACATGTCCTGGCTCTACACCTTCGCGGAGAAAGTTCCCTGGCAAGCTCTGCTCTTACTT 1961
Db 273 TGACATGTCCTGGCTCTACACCTTCGCGGAGAAAGTTCCCTGGCAAGCTCTGCTCTTACTT 214
QY 1962 CAGCCCTGGCCAGAGCCAGCCCAATGGCAAGACCTTCAGCGCTGCGGATCAACACCGT 2021
Db 213 CAGCCCTGGCCAGAGCCAGCCCAATGGCAAGACCTTCAGCGCTGCGGATCAACACCGT 154
QY 2022 CCGCATCTAGTCCAGGCGAAGAGACCAACACCTTCCTGGGACCACTGCGCCTGCAAGA 2081
Db 153 CCGCATCTAGTCCAGGCGAAGAGACCAACACCTTCCTGGGACCACTGCGCCTGCAAGA 94
QY 2082 GCCCTGCCCAAGAGATAGAACCTGGACTCCAGCCACCTGGCCACTGGAGACCTCA 2141
Db 93 GCCCTGCCCAAG-AGATAGAGACCTGGACTCCAGCCACCTGGCCACTGGAGACCTCA 35
QY 2142 GGCCAGTTGTTTACCTCCAGCTCCAGTCTGTA 2175
Db 34 GGCCAGTTGTTTACCTCCAGCTCCAGTCTGTA 1
RESULT 10
US-09-864-761-23962/c
; Sequence 23962, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04

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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 43117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23962
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC02262.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
; OTHER INFORMATION: EST HUMAN HIT: BE315402.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q02084, EVALUE 5.00e-28
; OTHER INFORMATION: NT HIT: g111423970, EVALUE 0.00e+00
US-09-864-761-23962

Query Match 11.3%; Score 431; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.6e-110;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GTACTGGGCTCCACTACTCGGAGGTGGTGGCGGAGAACCCAGTGGGTGATCGGGC 1702
DB 431 GTAGTGGGCTCCACTACTCGGAGGTGGTGGCGGAGAACCCAGTGGGTGATCGGGC 372
QY 1703 TGGCACACGAAGCCGCAAGCCGAGGAGGATCCAGATCCAGTCCAGCCAGCCGGCTTCT 1762
DB 371 TGGCACACGAAGCCGCAAGCCGAGGAGGATCCAGATCCAGTCCAGCCAGCCGGCTTCT 312
QY 1763 ACTGATCGTGTATGCACGATGGCAACAGTACAGCGCTGCAAGGAGCCCTGAGCGCGC 1822
DB 311 ACTGATCGTGTATGCACGATGGCAACAGTACAGCGCTGCAAGGAGCCCTGAGCGCGC 252
QY 1823 TTAAGCTCCGGACAGCTTGACAGGTGGGTGCTTCTCTGACTATGACCAAGGCTTGC 1882

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DB 251 TTAAGCTCCGGACAGCTTGACAAAGTGGGTGCTTCTCTGGACTATGACCAAGGCTTGC 192
QY 1883 TCATCTTTTACAATGCTGATGACATGTCCTGGCTCTACACCTTCGCGAGAAAGTTCCCTG 1942
DB 191 TCATCTTTTACAATGCTGATGACATGTCCTGGCTCTACACCTTCGCGAGAAAGTTCCCTG 132
QY 1943 GCAAGCTCTGCTCTTACTTTCAGCCCTGGCAGAGCCAGGCAATGGCAAGACGTTTCAGC 2002
DB 131 GCAAGCTCTGCTCTTACTTTCAGCCCTGGCAGAGCCAGGCAATGGCAAGACGTTTCAGC 72
QY 2003 CGCTGGCGATCAACACCGTCCGATCTAGTCCAGGAGGAGGAGACCAACACCTTCTCTGG 2062
DB 71 CGCTGGCGATCAACACCGTCCGATCTAGTCCAGGAGGAGGAGACCAACACCTTCTCTGG 12
QY 2063 ACCACTGCCAC 2073
DB 11 ACCACTGCCAC 1

RESULT 11
US-10-094-749-1459
; Sequence 1459, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1459
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1459

Query Match 4.2%; Score 160.2; DB 16; Length 2045;
Best Local Similarity 48.9%; Pred. No. 1.3e-33;
Matches 663; Conservative 0; Mismatches 648; Indels 44; Gaps 7;

QY 616 CTCAGGACGAGCTGCTGTGCTTCCATCTGCCTGAGCATCTACAGGACCCGCTGAGCCTG 675
DB 229 CTGGAGGACCGGCTTCAGTGTCCCATCTGCCTGGAGGTTCTCAAGGAGCCCTGATGCTG 288
QY 676 GCGTGGAGCACTACTTCTGCGCGCTGTCATCAGGAGCACTGGGTGGGAGGAGCG 735
DB 289 CAGTGTGGCCACTCTTACTTGCAGGGGCTGCCTGTTCCTGTCCCTGCACCTGGATGCC 348
QY 736 CAGGCGCGCCGCACTGCGCCGAGTGGCGGCGACGTTCCGCGAGCCCGCGCTGGCGCCC 795
DB 349 GAG-----CTGCGCTGCCCCGTGTGCGGCGAGGCGGTGGATGGCAGCAGCTCCCTGCCC 402

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QY	796	AGCCTCAAGCTGGC	AAACATCGTGGAGCGCTACAGCTCCTTCCCGCTGGACGGCATCTCTC	855
Db	403	AACGTCTCCCTGGCCAGGGTGATCGAAGCCCTTGAG--CTCCCTGGGACCCGAGACCCA	460	
QY	856	AACGGCGGCGCGCGCGGACCCCTGCCAGAGGCGACGACAAGGTCAAGCTCTTCTTGGCTC	915	
Db	461	AGTCTGCGTGCACACCGGAACCGC-----TCAGCCTTTCTGCGAG	504	
QY	916	ACGGACGGCGCTTCTCTGCTTCTTCTGCGAGAGCCTGCACTGCACGAGCAGCATCAG	975	
Db	505	AAGGACAGGAGCTCATCTGTGGCTCTGTGGCTCTCGGCTCCCAACACCAACCCG	564	
QY	976	GTCAACCGGATCAAGACGCTTTCGACGAGCTCGACAGGAGCTGAAAGCAACAACTTCAG	1035	
Db	565	GTACGCGCGCTTCCACCGTCTACGCCGATGAAGGAGAGCTCGACGCCCTCATCTCT	624	
QY	1036	GCCCTTCAAGACAGCAGCGGGAAACACACGGAAGCGCTCGAGTGTCTAAGCGCAACTG	1095	
Db	625	GAGCTGAAGCAGGAGCAGAAAAGGTGGATGAGCTCATCGCAAACTGGTGAACACCGG	684	
QY	1096	GCGAGACAAAGTCTTCCACAAAGAGCTTCGACCACTATCGGAGAGCCTTCGAGCGG	1155	
Db	685	ACCCGAATCTCAATGAGTCCGATGTTTTCAGCTGGGTGATCCCGCGAGTTCAGGAG	744	
QY	1156	CTGCACCGGTGCTCGGTGAACGCCACCGAAGGCCATGCTAGAGGAGCTGGAGCGGACAG	1215	
Db	745	CTGCACCACTGGTGATGAGGAGAGGCCCGCTGCTGGAGGGAT--AGGGGGGTCAAC	802	
QY	1216	GCCGCACTGACCGGACATCGACAGAAAGTCCAGCGCTACAGCAGCAGCTGCGCAAG	1275	
Db	803	ACCCGTGGCTGTGGCTCCCTGGACATGACAGCTGGAGCAGGCCACGAGGAACCCGGGAG	862	
QY	1276	GTCAGAGGGAGCCAGATCTTCGAGAGCGGTGCTGAACCGACCGGACACACTTTC	1335	
Db	863	CGGCTGGCGCCAGCCGAGTGTGTCTGGAAAGTTTGGCAATCAGAGACCACCAAGTTTC	922	
QY	1336	CTGGCTGG-----GGTGGCTCACTGTCCGAGCGCTCAAGGGAAATTCATGAGACC	1389	
Db	923	ATCCGGTTCACACTCCATGGCTCCAGAGCAGAGATGCCGAGGCCCGGCCCTTTAGAAGGC	982	
QY	1390	AACCTCAATATGAAGATCTCCGACCTCAAGTACACAGGCCCTCGCAGTACACCATC	1449	
Db	983	GCATTCACCCCATCTCTCTTCAAGCCAGGCGCTCCACCAGGCTGACATCAAGCTGACCGTG	1042	
QY	1450	TGGAAGTCCCTGTTCCAGGACATCAACCCAGTGCAGCCGCCCTTAACCTTGGACCCGGGC	1509	
Db	1043	TGGAAAGGCTCTTCGGAAAGTTTTCGACGCCCGGAGCCTCTCAAGTTGGACCCCTGCC	1102	
QY	1510	ACAGCCCAACGCGCTGATCCTGTGGAACGATGACCAATGTGGCTTACGGAACCTTG	1569	
Db	1103	ACTGCCCAACCACTCTCTGGAGCTCTC---CAAAGGGCAACAGGTGTGTCAGTCCGGGCTT	1159	
QY	1570	CACCCAGAGCCACTGCAGGACTGCCAAAGCGCTTCGATGTGGAGTGTCCGTGCTGGGT	1629	
Db	1160	CTGGCCCAAGCGGAGCCAGCCAGCTGAGCGCTTCGATACAGCACTCGCTCTGGCC	1219	
QY	1630	TCTGAAGCTTTCAGTAGTGGGCTCCACTACTTGGAGTGTGTGPGCGGAGAGAACCCAG	1689	
Db	1220	AGCCCGGCTTCTCTCGCGCGCCACTACTCTGGAGTGTGTGTTGGCAGCAAGAGCGAC	1279	
QY	1690	TGGGTGATCGGCTGGCACAGAAAGCCGACAGCGCAGAGGCGACATCCAGATCCAGCCC	1749	
Db	1280	TGGCGCTTGGGGGTCAACAAGGGCAGCAGCGCGTGAAGGCAAGCTGAACAGTCCCCC	1339	
QY	1750	AGCCCGGCTTCTACTGTCATCGTGATGACGATGGCAACCAAGTACAGCGCTTCACGGAG	1809	
Db	1340	GAGCACGGCGTGTGCTGATCGGCTGGAAGGGGCCGGGTGTACGAAGCCTTTGCTGTC	1399	
QY	1810	CCCTGGAACGGGCTTAAAGTCCGGGACAAAGCTTGACAGGTGGGTGTCTCTCTGACTAT	1869	
Db	1400	CCCCGGGTACCCCTGCCCGTGGCGGCCACCCCAACCGCATTCGGGCTTACTCTGCACTAT	1459	

Qy	1870	GACCAAGGCTTGCTCATCTTCTCAATG-----CTGATCAGATGCTCTGGCTCTAC	1921
Db	1460	GAGCAGGGCGAACTCACCTTTCTTCGATGCGGACCGGCCGATGACCTGGCGCGCTCTAC	1519
Qy	1921	ACCTTCGGCAGAGTTCCCTGCGCAAGCTCTGCTC	1955
Db	1520	ACCTTCAGCGCCGACTTCCAGGGCAAGCTCTACC	1554
RESULT 12			
US-09-764-868-418			
; Sequence 418, Application US/09764868			
; Patent No. US20020168711A1			
; GENERAL INFORMATION:			
; APPLICANT: Rosen et al.			
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
; FILE REFERENCE: PT232			
; CURRENT APPLICATION NUMBER: US/09764,868			
; CURRENT FILING DATE: 2001-01-17			
; Prior application data removed - refer to PALM or file wrapper			
; NUMBER OF SEQ ID NOS: 1510			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 418			
; LENGTH: 1394			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-764-868-418			
Query Match 3.6%; Score 136.4; DB 9; Length 1394;			
Best Local Similarity 54.9%; Pred. No. 4.9e-27;			
Matches 269; Conservative 0; Mismatches 221; Indels 0; Gaps 0;			
Qy	1482	GCCAGCGCCCTTAACCTTGGACCCGGGACGAGCCACAGGGCCCTGATCTCTGTCGAGGA	1541
Db	45	GCCAGCGGATGTGACCCCTGGACCCCTGAGACAGCTCATCTTAACCTGTCTGTGAGAGGA	104
Qy	1542	CTGCACCANTTGTGGCTTACGGCAACTTGCACCCACAGCCACTGCGAGGACTCGCCAAAGCG	1601
Db	105	TGCTAAGAGCGTCAAGTTCTGTGGAGACAGACTCGGGATCTCCCTGACACACCAAGCG	164
Qy	1602	CTTCGATCTGGAGGTGTCGGTGTCTGGGTCTTGAAGCTTCAAGTGTGGCGTCCACTACTG	1661
Db	165	TTTCACCTTCTACCCCTTGGCTCTGGCTACTGAGGGTTTACCTCAGGTGACACTACTG	224
Qy	1662	GGAGTGTGTGTGGCGGAGAGACCCAGTGGGTGATCGGGCTGGCACAGGCGCGAAG	1722
Db	225	GGAGTGTGAGGTGGCGGACAGACCCACTGGGCGAGTGGTGTATGCCGGGACTCCGTGAG	284
Qy	1722	CGCAGAGGCGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGTCACTGTCGATCAGGA	1781
Db	285	CCGAAGGCGGAGTTGACTCCACTCCCTGAGACTGGCTACTTGGGGGTGCGGCTATGGAA	344
Qy	1782	TGGCAACCAAGTACAGCGCTTGCAGGAGCCCTGGACGGGCTTAAAGTCCGGGACAAGCT	1841
Db	345	TGGGACAAATATGAGCCACCCACACACCTTTTACCCCTTTGACATCAAGGTGAAACC	404
Qy	1842	TGACAAGGTGGGTGTCTTCCTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGA	1901
Db	405	CAAAGCGGTAGGCATATTCTCTAGACTATGAGCCGGGACACTGTCTTTTCAATGCTCAC	464
Qy	1902	TGACATGTCTCGGCTCTACACCTTCCGGGAGAAAGTTCCCTGGCAAGCTCTGCTCTTACTT	1961
Db	465	AGACCGCTCTCATATCTACACCTTCTCACTGATACTTTTACTGAGAAACTTTGGCCCTCTT	524
Qy	1962	CAGCCCTGGC	1971
Db	525	CTACCCAGGC	534

RESULT 13

; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Kyle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyun
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 277
; LENGTH: 3038
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1557)
US-10-120-988-277

Query Match
Best Local Similarity 54.5%; Score 132.4; DB 16; Length 3038;
Matches 265; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

QY	1486	GCGCCCTAACCTTGGACCGGGACAGCCACAGCGCTGTGTCGGAGCTGC	1545
Db	1009	GCGGANGTACCTTGGACCGGGACAGCTCATCTAACCTGTGTCGGAGCTGC	1068
QY	1546	ACCATTTGGCTTACGGCACTTGCACCCACAGCCATGCGAGCTCGCCAAAGCGTTC	1605
Db	1069	AAAGCGTCAAGTTCGTGGAGACAAGACTCGGGATCTCCCTGACACACAAAGCGTTC	1128
QY	1606	GATGTGGAGTGTGGTGTCTGAAGCCTTCAAGTGTGGCTTCACTACTTGGGAG	1665
Db	1129	ACCTTCTACCTTGGCTGTGGCTTCACTGTGGGTTTCACTGAGTGCAGCTACTTGGGAG	1188
QY	1666	GTGGTGTGGGAGAGACCAAGTGGTGTATCGGGTGGCAACAGCGCGCAAGCCGC	1725
Db	1189	GTGGTGTGGGAGAGACCAAGTGGTGTATCGGGTGGCAACAGCGCGCAAGCCGC	1248
QY	1726	AAGGGCAGCATCCAGATCCAGCCAGCGCGGCTTCTACTGATCGTGTGACGATGGC	1785
Db	1249	AAGGGCAGTGTACTCCACTCCCTGAGACTGGCTACTGGCGGTGTGGATGGG	1308
QY	1786	AACCAATACAGCGCTTGCAGCGGACCCCTGGACCGGCTTAACTCCGGGACAAAGTTGAC	1845
Db	1309	GACAAATATGACGCCACCAACACCTTTTACCCCTTTGACATCAAGTGAACCAAG	1368
QY	1846	AAGTGGGTGTCTTCTGGACTATGACCAAGGCTTGTCTATCTTCAATGCTGATGAC	1905
Db	1369	CGGTAGGCAATATCTAGACTATGAGCGGGACACTGTCTTTTCAATGCTGACAGAC	1428
QY	1906	ATGTCTGTGCTCTACACCTTCCGCGAGAGTTCCCTGGCAAGCTCTGCTTACTTTCAGC	1965
Db	1429	CGCTCTCATATCTACACTTCTAGTACTTTTACTTGAGAAATTTGGGCCCTCTTCTAC	1488
QY	1966	CTGGC 1971	
Db	1489	CCAGGC 1494	

RESULT 14

US-10-104-047-103
; Sequence 103, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA

; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 1904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-103

Query Match
Best Local Similarity 45.7%; Score 122.8; DB 16; Length 1904;
Matches 519; Conservative 0; Mismatches 602; Indels 15; Gaps 2;

QY	893	ACAAGGTCAAGCTCTTCTGCTCAGGACCGCGGCTTCTCTGCTTCTTCTGCGACGAGC	952
Db	1	ACCGCTGAGCATCTACTGCGAGCAGACCGCGGCTGCTGCGGAGTGTGCGCTCAC	60
QY	953	CTGCATCTGCAGCAGCATCAGCTCACCGCATCGAGCGCTTCGACGAGTGCAGA	1012
Db	61	TCGCTCGCACCGCGCTCATCGCTCTCTGCTGCGCGGAGGCCACGACGCTCAAGA	120
QY	1013	GGGAGCTGAAGGACCACTTCAAGCCCTTCAAGACAGCGAGCGGGAACACACCGAAGCGC	1072
Db	121	CACAGCTGCCACAGCAGAACTGCAGCTGCAGGAGGATGCATCGTAAAGGAGAGTG	180
QY	1073	TGCAGCTGCTCAAGCAGCAACTGCGGAGACCAAGTCTTCCACCAAGAGCTTGGGACCA	1132
Db	181	TGGCTGTCTGGAGCATCAGCTGTGGAGGTGGAGGAGACAGTGCCTCAGTTCGCGGGG	240
QY	1133	CTATCGCGGAGGCTTCGAGCGGCTGCACCGGCTGCTGCTGAGACGCCAGAGCCATGC	1192
Db	241	CCGTGGGGAGCAGCTGGGCAAGATCGGGTGTCTTGGCTGCATCGAGGGGTCTCTTG	300
QY	1193	TAGAGGAGTGGAGGGGACACCGCGCGCACGCTGACCGACATCGACGAGAAAGTCCAGC	1252
Db	301	ACCGGAGGAGCAGCGGTGTACGGGTGAGGACGAGGCTTGGCGCGGAGCTGGGGA	360
QY	1253	GCTACAGCAGCAGCTGCGCAAGGTCCAGGAGGAGCCAGATCTCTGACGAGGGGTGG	1312
Db	361	GCTGAACTCTTACCTGGAGCAGCTCGGCAGATGGAGAAGGTCTCTGGAGAGGTGGCG	420
QY	1313	CTGAACCCGACCGGCACACCTTCTGCTGGGTGGCTCACTGTCCGAGCGCTCAAGG	1372
Db	421	ACAAGCGCAGACTGAGTTCTCATGAATACTGCTGTGTGACCGACGAGCTGCAGAAGA	480
QY	1373	GAAATATCATGAGACCACTCAATATGAAGCTTCCGACCTCCAAAGTACACAGGCC	1432
Db	481	TCCTGGCAGAGTCTCCCGCCACCGCGCTGTGACATCCAGCTGCCAATATCTCAGATG	540
QY	1433	CCCTGCAGTACCACTCTGGAAGTCCCTGTTCCAGACATCCACCCAGTCCAGCGCCC	1492
Db	541	ACTTCAATTCAGGTGTGGAGAAATGTTCCGGGCTCTGATGCGCAGCGCTGGAGGAGC	600
QY	1493	TAACTCTGACCGCGGCACAGCCCAAGCGCTGATCTGTCGGAGCAGTGCACCATTTG	1552
Db	601	TGACCTTTGACCGAGCTCTGCGACCCGAGCTGTGTGTGTCTTCTCTGCGCGCGCG	660
QY	1553	TGGCTTACGGCACTTGCACCCACAGCCACTCAGGACTCGCCAAAGCGCTTCTGATGTG	1612
Db	661	TGGAGTGTCTGGGGCAGAAAGCGCGCGGAGGACCCCGCGCCAGTTCGACAAAG	720
QY	1613	AGGTGTCTGCTGCTTCTGAAGCTTTCAGTGTGGCTTCCACTACTTGGAGGTGTGG	1672
Db	721	CGTGGCGGTGTGGCGCACCGAGAGCTCTCCAGGGCGAGCACTACTTGGAGGTGGATG	780
QY	1673	TGGCGGAGAAAGCCAGTGGGTGTGTCGGCTGGCACACGAAAGCCGCAAGCCGCAAGGCA	1732
Db	781	TTGGCGACAAAGCGCGCTGGGCGCTGGGCGGTGATCGCGCCGAGGCCCGCGCGGCG	840

1733 GCATCCAGATCCAGCCGCGGCTTCTACTGCATCGTATGACGATGGCA----- 1786
1779 CGATGGCAACCACTAGCGGCTTGAACGCGGCTTAAACGCTCCGGGACAA 1838
1427 GAACCAAACTGATCTAAGGCTCTGGATTTGGCTTTCTTTCAGTCTGACACTGACTAACAA 1486
1839 GCTTGACAAGGTGGGTCTCTTCTTGGAATATGACCAAGGCTTGTCTATCTTCTAACAATGC 1898
1487 CCTCGACAAGGTGGGCATATACCTGGATTATGAAGGAGGACAGTTGTCTTCTTACAATGC 1546
1899 TGATGACATGTCCTGGCTCTACACCTTCCGGGAGAAAGTTCCCTGGCAAGCTCTGCTCTTA 1958
1547 TAAACCATGACTCACATTTACACCTTTCAGTAAACACTTTTCATGGAGAAACTTTATCCCTA 1606
1959 CTTTCAGCCTGGCCAGAGCCGCAATGGCAAGAACG 1996
1607 CTTTGGCCCTGCTTAAATGATGATAGAGAGATAAAG 1644

Search completed: July 31, 2004, 23:28:10
Job time : 1590 secs

RESULT 15
US-09-731-872-225
; Sequence 225, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78-US3-REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 225
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 171..1670
US-09-731-872-225

Query Match 3.2%; Score 122; DB 9; Length 1739;
Best Local Similarity 51.9%; Pred. No. 6.1e-23;
Matches 300; Conservative 0; Mismatches 275; Indels 3; Gaps 1;
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1070 CCAGTACAAGGTCCTATCCAGTACATGTTATGGAGGAAATGACGACACTCTCTGCC 1129
1479 AGTGCAGCGGCGCTAACCTGACCCGGGACAGCCACAGCGCTGATCCTGTGGA 1538
1130 AGGCTGTCTCCACTAACTTGGACCTTAAACAGCTACCCAAATCTGGTGTCTCCAA 1189
1539 CGACTGCACATTTGGCTTACGCACTTGCACCCACAGCCACTGCGGACTCGCCAAA 1598
1190 AAGCCAAACACGGCTCTGGCATGTGACATTAAGA---AGATAATGCTGATCTCTGA 1246
1599 GCGCTTTCGATGTGGAGGTGTCGGTGTGGTTCCTGAAGCTTCAGTAGTGGGCTCCACTA 1658
1247 GAGTTTGACTCAAGTGTGCTGTACTGGCTCAAGAGGCTTCAACCTCTGGAAGTGGTA 1306
1659 CTGGAGGTGCTGGTGGCGGAGAAAGCCAGTGGGTGATCGGGCTGCACACGAGCCGC 1718
1307 CTGGGAAGTAGAAGTAGCAAGAGACAAAATGGACAGTTGGAGTTGTCAGAGAAATCCAT 1366
1719 AAGCCGCAAGGCGAGCATCCAGATCCAGCCAGCGCGGCTTCTACTGTCATCGTGATCA 1778

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 12:05:13 ; Search time 247 Seconds
(without alignments)
8596.122 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggtcgctgacgaagc.....aaaaaaaaaaaaaaaaaaaa 3826

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
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5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	2.8	3416	2	US-08-724-394A-15
2	95.8	2.5	1782	4	US-09-220-132-158
3	94	2.5	7218	1	US-08-232-463-14
4	86.4	2.3	2926	2	US-08-724-394A-13
5	86.4	2.3	2970	4	US-09-566-921-105
6	82.8	2.2	3502	2	US-08-724-394A-16
7	81.6	2.1	53526	3	US-08-658-136-2
8	81.6	2.1	53577	3	US-08-658-136-1
9	80.4	2.1	152331	3	US-09-128-155-16
10	76.2	2.0	1926	2	US-09-249-585A-4
11	76.2	2.0	1931	2	US-09-130-114-2
12	75	2.0	4897	6	5196516-7
13	74.6	1.9	3470	4	US-09-486-147-2
14	74.4	1.9	320	3	US-09-165-264-7
15	74.2	1.9	16891	4	US-09-486-147-1
16	74	1.9	543	4	US-09-486-147-4
17	73	1.9	320	3	US-09-165-264-13
18	73	1.9	2882	2	US-08-724-394A-12
19	72.8	1.9	320	3	US-09-165-264-11
20	72.8	1.9	12001	1	US-08-458-568A-11
21	71.8	1.9	320	3	US-09-165-264-14
22	70.2	1.8	319	3	US-09-165-264-8
23	70	1.8	318	3	US-09-165-264-12
24	69.6	1.8	712	4	US-09-401-064-354
25	63.6	1.7	77536	4	US-09-410-551B-1
26	62.6	1.6	2561	4	US-09-616-289-48
27	60.4	1.6	44377	2	US-08-804-227C-7

28	60.4	1.6	44377	2	US-08-804-198-1	Sequence 1, Appli
29	60	1.6	3227	4	US-09-620-312D-103	Sequence 103, App
30	59.4	1.6	697	3	US-09-040-984-17	Sequence 17, Appl
31	59.4	1.6	697	4	US-09-123-912-17	Sequence 17, Appl
32	59.4	1.6	697	4	US-09-643-597-17	Sequence 17, Appl
33	59.4	1.6	697	4	US-09-480-884A-17	Sequence 17, Appl
34	59.4	1.6	697	4	US-09-542-615A-17	Sequence 17, Appl
35	59.4	1.6	697	4	US-09-606-421B-17	Sequence 17, Appl
36	59.4	1.6	697	4	US-09-221-107-17	Sequence 17, Appl
37	58.6	1.5	1926	4	US-09-249-585A-2	Sequence 2, Appli
38	58.6	1.5	1926	4	US-09-410-399-3	Sequence 3, Appli
39	58.6	1.5	2580	3	US-09-050-863-2	Sequence 2, Appli
40	58.6	1.5	2580	4	US-09-359-081-2	Sequence 2, Appli
41	58.6	1.5	5452	2	US-09-130-114-1	Sequence 1, Appli
42	58.6	1.5	8705	4	US-09-647-344A-14	Sequence 14, Appl
43	58.6	1.5	9600	3	US-08-910-647-1	Sequence 1, Appli
44	58.6	1.5	9600	4	US-09-620-925-1	Sequence 1, Appli
45	58.6	1.5	10596	1	US-07-884-811-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-724-394A-15
; Sequence 15, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereeto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..3416
; OTHER INFORMATION: /note= "cDNA 44"
US-08-724-394A-15

Query Match 2.8%; Score 106; DB 2; Length 3416;
Best Local Similarity 53.8%; Pred. No. 7e-14;
Matches 242; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Qy 1482 GCCAGCGCCCTAACCTGGACCGGGGACAGCCACCAGCGCTGATCCTGTCGGACGA 1541
Db |||||
Qy 1373 GCCTGGGATGTGATCTGGATCCAAACAGCAACCCCATCTCTCTGTTCTGAGGA 1432
Db |||||
Qy 1542 CTGCACCATTTGGCTTACGGCAACTTGCACCCACAGCACTGCAGGACTCGCCAAAGCG 1601
Db |||||
Qy 1433 CCAGAGGAGTGTGACGGTGCCTAA--GGAGCCCCAGGATCTGCCAGACAACCTTGAGAG 1499
Db |||||
Qy 1602 CTTGATGTGAGGTGCTGCTGGTTCAGAGCTTCAAGCTTCAAGTGTGCTGCTCACTG 1661
Db |||||
Qy 1490 ATTTAAATGGCAATTTATTTGTTCTCGGCTGTGAGAGCTTCAATATCAGGAGACATTA 1549
Db |||||
Qy 1662 GGAGTGTGTGTCGGGAGAGACCCAGTGGTGTATCGGGCTGGACAGCGCGCAAG 1721
Db |||||
Qy 1550 GGAGTGTGAGTGTGAGGACAGGAAGAGTGCATATAGGGGTGTCAGTAAGAATGTGA 1609
Db |||||
Qy 1722 CCGAAGGCGAGCATCCAGATCCAGCCAGCGCGGCTTCTACTGATCGTGTGATGACGA 1781
Db |||||
Qy 1610 GAGAAAGGCTGGGTCAAAATGACACCTGAGATGATCTGGACTATGGGCTGACTGA 1669
Db |||||
Qy 1782 TGGCAACAGTACAGCGCTGCAGCGAGCCCTGGACGGGCTTAACGTCCGGGACAGCT 1841
Db |||||
Qy 1670 TGGCAATAGATATCGGACTTAACTGAGCCAGCAACCACTGAACTTCTTAAAGCCCC 1729
Db |||||
Qy 1842 TGCAAGTGGGTCTTCTCTGGACTATGACCAAGGCTTGTCTCACTTCTCAATGCTGA 1901
Db |||||
Qy 1730 TAAGAAATGGGGTCTTCTCTGGACTATGAGCTGGAGATATCTCATTTCAATGCTGT 1789
Db |||||
Qy 1902 TGACATGTCCTGCTTACACTTCCGGCA 1931
Db |||||
Qy 1790 GGATGGATCGCATATTCATCTTCTCTGA 1819
Db |||||

RESULT 2
US-09-220-132-158
; Sequence 158, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; FILE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/069,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-158

Query Match 2.5%; Score 95.8; DB 4; Length 1782;
Best Local Similarity 52.6%; Pred. No. 9.8e-12;
Matches 233; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

Qy 1484 CAGCGCCCTAACCTGGACCGGGGACAGCCACCAGCGCTGATCCTGTCGGACGACT 1543
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Qy 1178 CAGTGGAGTGTGACTCTGGACCCAGACAGCGGCTACCCAGCGCTGATCTCTGTGATAATC 1237
Db |||||
Qy 1544 GCACCATTTGGCTTACGGCACTTGCACCCACAGCACTGAGGACTGCGCAAGCGCT 1603
Db |||||
Qy 1238 TGGCGGAAGTGGGTACAGTTAC---CTCCACAGGAGCTGCTGACAAACCCCGAGAGT 1294
Db |||||

Qy 1604 TCGATGTGGAGTGTGCTCGGTCTTGAAGCGCTTCAGTAGTGGGCTCCACTACTGGG 1663
Db |||||
Qy 1295 TCAATCTGTTTCCCTGTGTCTTGGGCTCTCCATGCTTCATCGCGGAGACATTTATGGG 1354
Db |||||
Qy 1664 AGTGTGTGTGGCGGAGAACCCAGTGGGTGATCGGGCTGGCACAGAAAGCCGCAAGCC 1723
Db |||||
Qy 1355 AGGTAGAGGTGGGAGATAAAGCCAAAGTGGACCATAGGTGTCTGTGAAGACTTCAGTGTGCA 1414
Db |||||
Qy 1724 GCAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGCTCGTGTGCAAGATG 1783
Db |||||
Qy 1415 GAAAGGTGGAGTAACCTCAGCCCCCAGAAATGATTTCTGGGCAAGTGTCTTTTGTGGTATG 1474
Db |||||
Qy 1784 GCAACCAAGTACAGCGCTGACCGAGCGCTTAAAGTCCGGGACAAAGCTTG 1843
Db |||||
Qy 1475 GGAAGAAATATTGGGCTTCTTACCTCCCAATGACTGCGCTACCCCTGGGACCCGCTCC 1534
Db |||||
Qy 1844 ACAAGTGGGTGTCTTCTCGGACTATGACCAAGGCTTGTCTCATCTTCTTCAATGCTGATG 1903
Db |||||
Qy 1535 AGCGGTGGGATTTTCTTGGACTATGATGCTGGTGGAGTCTCCTTCTTCAACAGTGCAG 1594
Db |||||
Qy 1904 ACATGCTCTGCTTACACCTTC 1926
Db |||||
Qy 1595 AGAGGTGTACACCTTCACTTTC 1617
Db |||||

RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFELINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14


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Query Match          2.5%; Score 94; DB 1; Length 7218;
Best Local Similarity 2.6%; Pred. No. 3.9e-11;
Matches 10; Conservative 257; Mismatches 117; Indels 0; Gaps 0;
QY 213 GGGATTTCAGCCCTTAAGGCTCCACCCGCTCGGATCCCTTCGCCAGCTCCTA 272
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1056 GAGCTTGCATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1115
QY 273 TCCCTTAGGACTGCCGCCCTAGAACCTCCCGTCAGGATCCGCTCCAGCCGC 332
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1116 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1175
QY 333 TCACAGCTCTCCAGCCGCTAGCTGAGTCCGCTAGCTGAGCTGAGCTGAGCT 392
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1176 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1235
QY 393 CGGCTGGGCTCCAGCGAGTCTCAGCGCGCAGCCCTTCCTCGGCTTACCTTC 452
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1236 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1295
QY 453 GACAGCACCCCTCCCTTCTCGGTAGCTCTACCCCTGCTGTCGGGCTGTCGCC 512
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1296 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1355
QY 513 CGCCAGAGCTGCTGCTGCTCGCTCGAGCGGCGGCTCTCTCAGCGCGCCCTGCC 572
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1356 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1415
QY 573 TCGGGCCCTCTCTGCTGCC 596
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1416 YYYYYYYYYYYYYYYYYGTACC 1439
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RESULT 4
US-08-724-394A-13
; Sequence 13, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 13:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2926
; OTHER INFORMATION: /note= "cDNA 29"
US-08-724-394A-13

Query Match          2.3%; Score 86.4; DB 2; Length 2926;
Best Local Similarity 52.7%; Pred. No. 1.3e-09;
Matches 236; Conservative 0; Mismatches 206; Indels 6; Gaps 2;
QY 1483 CCAGCGCGCCCTAACCCCTGGACCCCGGCACAGCCACAGCGCTGATCCTGTCGAG 1542
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1186 CTGCGGATGTGATTCTGGATCCAGACAGCGCAACGCCATCCTCCTTCTTCTGAGGAC 1245
QY 1543 TGCACCATTTGTGCTTACGGCAACTTGACCCACAGCCACTGAGGACTCGCAAGCGC 1602
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1246 CAGAGGAGTGTG---CAGCGTGTGAAAGAGCGCGGATCTGCCAGACAAACCTGAGAG 1302
QY 1603 TTTCGATGTGAGGTGTGCGTGTGCTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTG 1662
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1303 TTGATGCGGTACTGTGCTTCTGCTGTGAAACTTTCATCAGGGAGACATTAATCTG 1362
QY 1663 GAGGTGCTGTGCGGAGAGACCCAGTGGTGTGTCGGCTGGCAC---ACGAAGCCGA 1719
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1363 GAGGTGGAAGTGGGAGACAGAAAGAGTGCATATTGGGGTATGTAGTAAGAACGTGGAG 1422
QY 1720 AGCCGAGGAGGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGATGCTGATGCAC 1779
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1423 AGGAAAAAGTGGGTCAAAATGACCCGGAACCGGATCTGGACTATGGGCTTGACT 1482
QY 1780 GATGCAACAGTACAGCGCTGACGAGCCCTGACGCGGCTTAACGTCGGGACAAG 1839
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1483 GATGGGATAAGTATCGGCTCTACTGAGCCAGAACCACTGAACTTCTGAGCCT 1542
QY 1840 CTTGACAAGTGGGTGTCTTCTGGAATGACCAAGGCTTGTCTATCTTCTACAATGCT 1899
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1543 CCTAGGAAAGTGGGATCTTCTGGAATGAGCTGAGAGATCTCGTCTTCTATAATGC 1602
QY 1900 GATGACATGTCTGCTCTACACCTTCC 1927
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1603 ACAGATGATCTCATATCTACACCTTTC 1630
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RESULT 5
US-09-566-921-105
; Sequence 105, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora M.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 105
; LENGTH: 2970
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6682888 902288.16
; NAME/KEY: unsure
; LOCATION: 2113-2202
; OTHER INFORMATION: a, t, c, g, or other
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US-09-566-921-105

Query Match 2.3%; Score 86.4; DB 4; Length 2970;
Best Local Similarity 52.7%; Pred. No. 1.3e-09;
Matches 236; Conservative 0; Mismatches 206; Indels 6; Gaps 2;
QY 1483 CCAGCGCCCTAACCCCTGGACCGGGACAGCCACAGCCGCTGATCCTCTCGGAGAC 1542
Db 1220 CTTGGGATGATCTGGATCCAGACAGGCAACGCCATCCTCTGTTCTTGAGAC 1279
QY 1543 TGACCACTTGTGGCTTACGGCAACTTGACCCACAGCCACTGACGAGCTGCCAAAGCGC 1602
Db 1280 CAGAGGAGTGTG---CAGCGTGCTGAAGAGCGCGGGATCTGCCAGAACACCTTGAGAGA 1336
QY 1603 TTGATGTGAGGTGTGGTCTGGTCTGAGGCTTGAAGCTTCAGTAGTGGGTCCACTACTGG 1662
Db 1337 TTTGAATGGCGTTACTGTCTTGGCTGTGAAACTTCACATCAGGAGACATTAATCTGG 1396
QY 1663 GAGTGTGTGGTGGGGAGAGACCCAGTGGGTGATCGGCTGGGCAC---ACGAGCCGCA 1719
Db 1397 GAGTGTGAAGTGGGGACAGAAAGATGGCATATTTGGGTATGTAGTAAGACGTGGAG 1456
QY 1720 AGCCGCAAGGACGATCCAGATCCAGCCACAGCCACTGACGAGCTGCCAAAGCGC 1779
Db 1457 AGGAAAAAGGTGGCTCAAAATGACACCGGAGAACGATCTGACTATGGGCTGACT 1516
QY 1780 GATGCAACAGTACAGGCTGACCGAGCCCTGGAGCGGCTTAAGTCCGGGACAAG 1839
Db 1517 GATGGAATAGTATCGGCTCTCACTGAGCCGAGAACCAACCTTCTTGAAGCCT 1576
QY 1840 CTTGACAAAGTGGGTGTCTTCTGGACTATGACCAAGCTTGTCTCATCTTCTACATGCT 1899
Db 1577 CTTAGGAAGTGGGATCTTCTGGACTATGAGACTGGAGAGATCTGTTCTTAATGCC 1636
QY 1900 GATGACATGCTCTGGCTTACACCTTCC 1927
Db 1637 ACAGATGATCTCATATCTACACCTTTC 1664

RESULT 6

US-08-724-394A-16
; Sequence 16, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kromal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchibashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 3502 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..3502

OTHER INFORMATION: /note= "cDNA 32"

US-08-724-394A-16

Query Match 2.2%; Score 82.8; DB 2; Length 3502;

Best Local Similarity 52.2%; Pred. No. 8.8e-09;

Matches 233; Conservative 0; Mismatches 207; Indels 6; Gaps 2;

QY 1484 CAGCGCCCTTAACCCCTGGACCGGGACAGCCACAGCCGCTGATCTGTCGACGACT 1543

Db 1063 CTGCTGATGTGGTCTCGATCCAGACACCGCTCATCCGAGCTCTCTCTGTGAGAGACC 1122

QY 1544 GCACCATTTGGCTTACGGCAACTTGGACCCACAGCCACTGACGAGCTCGCCAAAGCGCT 1603

Db 1123 GGAGAGTGTGAGCGGGGGCCCT---ACAGGCAGAGAGTGCCTGACCAACCCAGAGAT 1179

QY 1604 TCGATGTGAGAGTGTGGGTCTGAGGCTTCTGAAGCCTTCAGTAGTGGGTCTCCACTACTGGG 1663

Db 1180 TCGACACTGACCTTGTCTCTGGATGGGAGAGCTTCGCTCAGGGAACATTAATCTGGG 1239

QY 1664 AGTGTGTGGTGGGAGAGACCCAGTGGGTGATCGGGCTGGGACACAGAACCCGCAAGCC 1723

Db 1240 AGTGTGAGTGGAAACGCTGATGTGTGACTGTGGGGGTCTGCAGACACAGTGTGAGA 1299

QY 1724 GCAGGCGCAGATCCAGATCCAGCCAGCCGCTTCTACTGTCATGTCGATGTCACGATG 1783

Db 1300 GGAAGGGGAGGTCTCTGCTGATTCCTCAGATGCTTCTGGACCTGGAGATG---TTTG 1356

QY 1784 GCACCACTAGTACAGCGCTCGACCGAGCCCTGGAGCGGCTTAAAGTCCGGGACAAGTTG 1843

Db 1357 GAAACCAATACCGGGCCCTGTCTCCCTGAGAGATTCCTCCCTTGAAGGAGTCCCTTT 1416

QY 1844 ACAAGTGGGTGTCTTCTCGACTATGACCAAGCTTGTCTCATCTTCTAATGCTGATG 1903

Db 1417 GCGGTTGGGCTTCTCTGACTATGAAGCTGGAGATGTCTCTCTTCTACAAATGAGGG 1476

QY 1904 ACATGCTCTGCTCTACACCTTCGC 1929

Db 1477 ACAGTACACATCTACATGTCCTCC 1502

RESULT 7

US-08-658-136-2

; Sequence 2, Application US/08658136

; Patent No. 6071717

; GENERAL INFORMATION:

; APPLICANT: KLINGER, KATHERINE W

; APPLICANT: LANDES, GREGORY M

; APPLICANT: BURN, TIMOTHY C

; APPLICANT: CONNORS, TIMOTHY D

; APPLICANT: DACKOWSKI, WILLIAM

; APPLICANT: GERMINO, GREGORY

; APPLICANT: QIAN, FENG

; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: ONE MOUNTAIN ROAD

; CITY: FRAMINGHAM

; STATE: MASSACHUSETTS

Patent No. 6627745
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as
APPLICANT: represented by the Secretary, Department of Health and Human
APPLICANT: Services
APPLICANT: Daniel L. Kastner
APPLICANT: Ivona Akseintijevich
APPLICANT: Michael Centola
APPLICANT: Zuoming Deng
APPLICANT: Raman Sood
APPLICANT: Francis S. Collins
APPLICANT: Trevor Blake
APPLICANT: P. Paul Liu
APPLICANT: Deborah Gumucio
APPLICANT: Robert I. Richards
APPLICANT: Darrell O. Rieke
APPLICANT: No. 6627745man A. Doggett
APPLICANT: Moraechai Pras
TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
TITLE OF INVENTION: FAMILIAL MEDITERRANEAN FEVER
FILE REFERENCE: 14014.0314U1
CURRENT APPLICATION NUMBER: US/09/486,147
CURRENT FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: PCT/US98/17255
PRIOR FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: 60/056,217
PRIOR FILING DATE: 1997-08-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3470
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
US-09-486-147-2

Query Match 1.9%; Score 74.6; DB 4; Length 3470;
Best Local Similarity 50.1%; Pred. No. 5.5e-07;
Matches 241; Conservative 0; Mismatches 234; Indels 6; Gaps 2;
QY 1493 TAACCTTGGACCGGGGACAGCCACAGGAGCTCGCAAGGCTTCTGATGCTGG 1552
Db 1799 TGATCTGGATGTCAGAAACCGCTTACCCCAACCTCATCTCTGATGATCTGAAGAGTG 1858
QY 1553 TGGCTTACGGCACTTCCACCCACAGCACTGCGAGGACTCGCAAGGCTTCTGATGCTGG 1612
Db 1859 TTAGACTTGAAC---AAGTGGAGAGGCTGCTGATGCTGCGCCGCAAGATTTGACAGCT 1915
QY 1613 AGGTGTCGTGCTGGGTCTTGAAGCCTTCAAGTGTGCGCTCCACTACTGGGAGGTGGTGG 1672
Db 1916 GTATCAATGTTCTGGGCTCTCCGAGTTTCTCTCTGCGCGCGTTACTGGGAGGTGGAGG 1975
QY 1673 TGGGGGAGAGACCCAGTGGGTGATCGGGTGGGACAGAGCGCGCAAGCGGCAAGGGCA 1732
Db 1976 TTGGAGACAAGACAGCATGATGCTGGGAGCCTTCAAGACATCCATAAGCAGGAAAGGGA 2035
QY 1733 GCATCCAGATCCAGCCCGCGGCTTCTACTGATGCTGATGCTGATGCTGATGCTGATGCTG 1792
Db 2036 ACATGACTCTGTCCGACAGAAATGGCTACTGGGTGGTGAATGATGATGATGATGATGATG 2095
QY 1793 ACAGCGCTCGACGAGCCCTGACGCGGCTTAACGTCGCGGACAAAGCTTTGACAAAGTGG 1852
Db 2096 ACCAGGCGTCCAGGTTTCCCGGACCGCGCTGTCTAATAAGAGAGCCTCCCAAGCGTGG 2155
QY 1853 GTGCTCTCGGACTATGACCAAGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1912
Db 2156 GCATCTCTGCTGACTACAGATGGAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2215
QY 1913 GGCTCTACACCTT---CCGCGAAGATTCCTCGGCAAGCTCTGCTCTTCTTCTTCTTCTTCT 1969
Db 2216 ACATCTATACATTCGCGAGCTGCTCTTCTCTGCGCGCTTCAACCTTCTTCTTCTTCTTCT 2275
QY 1970 G 1970

Db 2276 G 2276

RESULT 14

US-09-165-264-7/c
Sequence 7, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-7

Query Match 1.9%; Score 74.4; DB 3; Length 320;

Best Local Similarity 52.2%; Pred. No. 2.7e-07;
Matches 165; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 136 ACGGCTCGGCTGCTGCTCCCTCCCTCCAGGATTTCCCATCCCGAGCTTCTTCGCGCTGCC 195
Db 316 AGGCGATGGCTAGCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 257
QY 196 GCGACCGCGCCCGCCCGGAGTTTCGACCGCTTAAAGGCTTCACCGCGTCCGGGATCC 255
Db 256 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197
QY 256 CTTCTCCAGCTCTCTATCTTCTAGGACTGCGCGCGCGCGCTAGAACCTCCCGCTCAGGAT 315
Db 196 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 137
QY 316 CTGCTGCTCTCAGCGCTCAGCGCTCTCTCCCGCGCGCGCTTTCGCTTTCGCTGCTGCTG 375
Db 136 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 77
QY 376 CTTCTAGACTGCTCTCCGCGCTGCGGCTGCGGCTCCGACGAGTCTCAGCGCGGAGCCCTTCT 435
Db 76 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17
QY 436 GCGTTACCTCTCTTCC 451
Db 16 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17

RESULT 15

US-09-486-147-1
Sequence 1, Application US/09486147
Patent No. 6627745
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as
APPLICANT: represented by the Secretary, Department of Health and Human
APPLICANT: Services
APPLICANT: Daniel L. Kastner
APPLICANT: Ivona Akseintijevich
APPLICANT: Michael Centola
APPLICANT: Zuoming Deng
APPLICANT: Raman Sood
APPLICANT: Francis S. Collins
APPLICANT: Trevor Blake
APPLICANT: P. Paul Liu
APPLICANT: Deborah Gumucio
APPLICANT: Robert I. Richards
APPLICANT: Darrell O. Rieke
APPLICANT: No. 6627745man A. Doggett

```
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; TITLE OF INVENTION: FAMILIAL MEDITERRANEAN FEVER
; FILE REFERENCE: 14014.0314U1
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCI/US98/17255
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: 60/056,217
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16891
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: n = a, t, c, or g
US-09-486-147-1

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Best Local Similarity 49.9%; Pred. No. 1.1e-06;
Matches 240; Conservative 1; Mismatches 234; Indels 6; Gaps 2;

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QY 1553 TGGCTTACGGCACTTGACCCACAGCCACTGCGCAAGCGCTTCGATGTGG 1612
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Db 13963 TTAGACTTGGAAAC---AAGTGGGAGAGGCTGCCTGATGCCCGCAAGATTGACAGCT 14019
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QY 1613 AGGTGTCGTGCTGGTCTCTGAAGCCTTCAGTAGTGGCGCTCCACTACTGGAGGTGGTGG 1672
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QY 1673 TGGCGGAGAGACCCAGTGGGTGATCGGCTGGGCACACGAAAGCCGCAAGCGGCA 1732
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Db 14080 TTGGAGACAAGACAGCATGGATCCTGGGAGCCTGCAAGACATCCATAAGCAGGAAAGGGA 14139
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QY 1733 GCATCCAGATCCAGCCAGCCCGCGCTTCTACTGCATCGTGATGCAGATGGCAACCACT 1792
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QY 1793 ACAGCGCCTGCACGGAGCCCTGGACGCGGCTTAACGTCGGGACAAAGCTTTGACAGGTGG 1852
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QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1853 GTGTCTTCTGGACTATGACCAAGGCTTGCTATCTCTTACATGCTGATGACATGCTCT 1912
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14260 GCATCTTCTGGACTACAGATTGGAAGCATCTCTTTTACATATGTACAGCCRGATCCC 14319
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QY      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1970 G 1970
Db      |
Db 14380 G 14380
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Job time : 250 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:08:11 ; Search time 46 Seconds
(without alignments)
3233.658 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELLCSICLSIYQD.....GQSHANGKNVQPLRINTVRI 475

Scoring table: BLOSUM62

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Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1312	52.4	304	9	US-09-927-091-2
3	613	24.5	500	9	US-09-731-872-466
4	613	24.5	500	10	US-09-876-997-466
5	583	23.3	580	9	US-09-925-301-943
6	550.5	22.0	485	14	US-10-276-372-2
7	550.5	22.0	485	16	US-10-473-576-1
8	541.5	21.6	485	15	US-10-094-749-2615
9	501	20.0	471	15	US-10-104-047-3482
10	500	20.0	468	15	US-10-104-047-3664
11	499.5	19.9	4675	15	US-10-093-463-74
12	492	19.6	465	14	US-10-024-298A-97
13	492	19.6	465	14	US-10-042-211A-97
14	492	19.6	465	16	US-10-617-217A-97
15	489	19.5	465	14	US-10-024-298A-99

16	489	19.5	465	14	US-10-042-211A-99	Sequence 99, Appl
17	489	19.5	465	16	US-10-617-217A-99	Sequence 99, Appl
18	475.5	19.0	4691	15	US-10-093-463-72	Sequence 72, Appl
19	427.5	17.1	395	15	US-10-108-260A-4617	Sequence 4617, Ap
20	418	16.7	475	12	US-10-042-865-65	Sequence 65, Appl
21	418	16.7	475	14	US-10-000-897-78	Sequence 78, Appl
22	418	16.7	475	15	US-10-094-749-2393	Sequence 2393, Ap
23	414.5	16.6	488	12	US-10-221-625-82	Sequence 82, Appl
24	411	16.4	483	12	US-10-114-270-106	Sequence 106, App
25	409	16.3	579	12	US-10-042-865-6	Sequence 6, Appli
26	408	16.3	592	12	US-10-042-865-64	Sequence 64, Appl
27	407.5	16.3	474	15	US-10-104-047-3289	Sequence 3289, Ap
28	393	15.7	498	14	US-10-247-671-167	Sequence 167, App
29	388.5	15.5	194	9	US-09-764-868-1031	Sequence 1031, Ap
30	388.5	14.7	277	15	US-10-094-749-3098	Sequence 3098, Ap
31	364.5	14.6	413	12	US-09-978-360A-710	Sequence 710, App
32	364.5	14.6	413	14	US-10-319-763-198	Sequence 198, App
33	343.5	13.7	183	9	US-09-864-761-36547	Sequence 36547, A
34	341	13.6	630	16	US-10-408-765A-640	Sequence 640, App
35	341	13.6	630	16	US-10-317-277A-168	Sequence 168, App
36	340.5	13.6	438	15	US-10-262-445-34	Sequence 34, Appl
37	339	13.5	584	9	US-09-910-174A-16	Sequence 16, Appl
38	339	13.5	584	9	US-09-955-866-12	Sequence 12, Appl
39	339	13.5	584	9	US-09-896-738-18	Sequence 18, Appl
40	339	13.5	584	14	US-10-041-319-17	Sequence 17, Appl
41	339	13.5	584	16	US-10-648-593-157	Sequence 157, App
42	339	13.5	584	16	US-10-644-671-16	Sequence 16, Appl
43	334.5	13.4	333	15	US-10-104-047-2073	Sequence 2073, Ap
44	329	13.1	513	9	US-09-910-174A-18	Sequence 18, Appl
45	329	13.1	513	16	US-10-644-671-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-927-091-1
; Sequence 1, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: USPC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Human
US-09-927-091-1

Query Match	100.0%;	Score 2504;	DB 9;	Length 475;
Best Local Similarity	100.0%;	Pred. No. 7.1e-202;		
Matches 475;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MACSLKDELLCSICLSIYQDPSVLGCEHYFCRCITEHWVRQEAQAGARDCECRRTFAEP	60	
Qy	61	ALAPSLKLANIVRYSSFPDLAILNARRAAPQAHDKVKLCITDRALLCFCCDEPALH	120	
Db	61	ALAPSLKLANIVRYSSFPDLAILNARRAAPQAHDKVKLCITDRALLCFCCDEPALH	120	
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Db 181 AFERHLRLRERQKAMLELEADTARTLTDIEQKVORYSQQLRKVOEGAQILQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300
Db 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300
QY 301 PGTAHORLILSDCTIVAYGNLHPQLQDSPRFDEVSVLGSEAFSSGVHVEVVVAEK 360
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QY 361 TOWVIGLAHEAASRKSGSIQIOPSRGFCYIVMHDGNQYSACTEPWTRLNVDRKDKGVFL 420
Db 361 TOWVIGLAHEAASRKSGSIQIOPSRGFCYIVMHDGNQYSACTEPWTRLNVDRKDKGVFL 420
QY 421 DYDQGLLIFYNADMSWLYTFREKPGKLCVSFSPQSHANGKNVQPLRINTVRI 475
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RESULT 2

US-09-927-091-2
; Sequence 2, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Human
US-09-927-091-2

Query Match 52.4%; Score 1312; DB 9; Length 304;
Best Local Similarity 91.8%; Pred. No. 7.2e-102;
Matches 257; Conservative 2; Mismatches 5; Indels 16; Gaps 1;
QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQARDCEPCRRTFARP 60
Db 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQARDCEPCRRTFARP 60
QY 61 ALAPSLKLANIVERYSSFFPLDAILNARRAARPCQAHDKVKLCFLTDRLALCFCDPEPALH 120
Db 61 ALAPSLKLANIVERYSSFFPLDAILNARRAARPCQAHDKVKLCFLTDRLALCFCDPEPALH 120
QY 121 EQHQTGDDAFDELQRLKQALQALQDSEREHTEALQLLKRQLAETKSTKSLRTTIGE 180
Db 121 EQHQTGDDAFDELQRLKQALQALQDSEREHTEALQLLKRQLAETKSTKSLRTTIGE 180
QY 181 AFERHLRLRERQKAMLELEADTARTLTDIEQKVORYSQQLRKVOEGAQILQERLAETD 240
Db 181 AFERHLRLRERQKAMLELEADTARTLTDIEQKVORYSQQLRKVOEGAQILQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300
Db 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300

RESULT 3

US-09-731-872-466
; Sequence 466, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78-US3-REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pgm
; SEQ ID NO 466
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-872-466

Query Match 24.5%; Score 613; DB 9; Length 500;
Best Local Similarity 31.6%; Pred. No. 9.5e-43;
Matches 148; Conservative 83; Mismatches 222; Indels 16; Gaps 8;
QY 8 ELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQARDCEPCRRTFARPALAPSLK 67
Db 38 ELRCPLCNDWFRDPLMLSCGHNFCACIQDFWRLOAKE--TFCPECKMLCOYNNCTFNFV 95
QY 68 LANIVERYSSFFPLDAILNARRAARPCQAHDKVKLCFLTDRLALCFCDPEPALH--EQHQ 124
Db 96 LDKVKEIKKKPL-----LKGHPQCPHEGENIKLFSKPDGKLCIFQCKDARLSVQSK 149
QY 125 VTGIDDAFDELQRLKQALQALQDSEREHTEALQLLKRQLAETKSTKSLRTTIGSAFER 184
Db 150 FLQISDAVHFFMEELAIQQGQLETTIKELQTLRNNQKEAIAAHKENKHLHQHVSMEFLK 209
QY 185 LHRLLRERQKAMLELEADTARTLTDIEQKVORYSQQLRKVOEGAQILQERLAETDRHTF 244
Db 210 LHQFLHSKEKJLTRELREKALNEEMELNSLOEQECCLAKDMLVSIQAKTEQQNSFDF 269
QY 245 LAGVASLSERLKG--KIHET-NLTVEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 301
Db 270 LKDTITLLHSLEQGMKVLATRELISRKNLGQYKGPQYMWVREMQDTLCFGLSPLTLD 329
QY 302 GTAHORLILSDCTIVAYGNLHPQLQDSPRFDEVSVLGSEAFSSGVHVEVVVAEKT 361
Db 330 KTAHPNLVLSKQTSVWHGDI-KKIMPDDPFRFSDSSVAVLGSRGFTSGKWYWEVEVAKKT 388
QY 362 QWVIGLAHEAASRKSGSIQIOPSRGFCYIVMHDGNQYSACTEPWTRLNVDRKDKGVFLD 421
Db 389 KWTGVVRESIIRKSCPLTPEQGFLLRLRQNTDLKALDLSFSLTLLNNDKVGIYLD 448
QY 422 YDQGLLIFYNADMSWLYTFREKPGKLCVSFSPQSHANGKNVQPLRI 470
Db 449 YEGGQLSFYNAKTWTHIYTFSTFMKLYPYFCPLNDGR-ENKPELHI 496

RESULT 4
US-09-876-997-466
; Sequence 466, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78-US4-CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872

APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, KYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-326381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2615
LENGTH: 485
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2615

Query Match 21.6%; Score 541.5; DB 15; Length 485;
Best Local Similarity 28.5%; Pred. No. 9.4e-37;
Matches 148; Conservative 94; Mismatches 176; Indels 101; Gaps 17;
QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRCI-----TEHWVQEAQAGARDCEPCR 54
DB 9 AIVEEVACPICCTFTLRPEMSIDGHSFCHSLGLEIFGESQNW-----GYTCFLCR 61
QY 55 RTFAEPALAPSILANIVERYSSFFLDAILNARRAAPCOAH-DKVKLFCLTDRALLCFF 113
DB 62 APVQPNLRPNQLANVVEKVRLLRLHLPQMGKX-GDLCEHGEKLMKCKEDVLINCEA 119
QY 114 CDEPALHEQHVGTGIDDAFDELQRELDQALQDSEREHTEALQLLKRQLAET-KSSTK 172
DB 120 CSQSPHEAHSVVPMEDEVAVYKWLHEALHLK-KEQEEAWKLEVGERKRTATWKIQVE 178
QY 173 SLRTTIGAEFERLHRLREROKAMLEELADTARTLTDIEQKVQYISOQLR-----KVQEG 228
DB 179 TRKQSVWFEFYQRLLLEKKQPPH-RQLGAEVAAALASLOREAAETMQLNHSLEIQ 237
QY 229 AQLQERLAETDRHTELAGVASLSERLKGKIHEHTNLTYEDFPTSKYTGPIQYTIWKSFLQ 288
DB 238 SQVLWRMIAB-----LKERSQRPVR-----W--MLQ 261
QY 289 DI-----HPVPAAL-----TLDPGTAHORLLISDD 313
DB 262 DIQEVNRSKWSLQOPEPISLELTKDCRVGLRLREILKTYAADVRLDPDTAYSRLIVSED 321
QY 314 CTTVAVGNLHPQLOPSKPRFDEVSVLGSEASSGVHVEVVAEKTQWVIGLAHEAAS 373
DB 322 RKRWHYGDTH-QKLPDNPFRFYRNYIVLGSQCISGRHYHVEVEGDSRSEGLGVCKQNV 380
QY 374 RKGSIQIPSRGFYCIVMHDGNOYSACTEPWTRINVRDKLDKVGVDYDQGLLIYFNAD 433
DB 381 RKEVVLSPHYGFWTLRKNERYAGTDEYPLSLPVPVRRVGIFVDYEAHDSFINVT 440
QY 434 DM-SWLYTF-REKPPGKLCYSFPGOSHANGKNVQLRI 470
DB 441 DCGSHIFTPFRYPFGRLLFPYFPCYS-IGTNTNAPLAI 478

RESULT 9
US-10-104-047-3482
Sequence 3482, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1el full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3482
LENGTH: 471
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3482

Query Match 20.0%; Score 501; DB 15; Length 471;
Best Local Similarity 29.4%; Pred. No. 2.3e-33;
Matches 143; Conservative 91; Mismatches 208; Indels 44; Gaps 14;
QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVQEAQAGARDCECRTEAEPALA 63
DB 9 NLORESSCPICLEYLKDPTVINCENHFCRSCLSVSW--KDLDDTTPCPVCRFCFPYKSPR 66
QY 64 PSLKLANIVERYSSFFLDAILNARRAAP-----CQAHDK-VKLFCLTDRALLCFFCD 115
DB 67 RNPQLNLT-----IAQLQIRSKRKRQKENAMCKEKNQFLTLFCVKDLLEILCTQCS 120
QY 116 EPALHEQHVGTGIDDAFDELQRELDQALQDSEREHTEALQLLKRQLAETKSSTKSLR 175
DB 121 FSTKHQHYICPIKKAASYHREILGSLERPLRNRIERVEKVILOQSKSVLKKVYEYKR 180
QY 176 TTIGAEFERLHRLREROKAMLEELADTARTLTDIEQKVQYISOQLRQVQGAQLQER 235
DB 181 EINSSEFQIRLFLQNEQEMILRQIDEMNILA-----KLNENLVELSDVSTLKHLL 233
QY 236 LAETDRHTELAGVASLSERLKGKIHE-TNLTYED-----FPTSKY--TGPIQYTIWKSFLQD 289
DB 234 LREVEGKSVQSNLELLTQ-AKSMHKKYQNLKCPLEFSFRLTKYGFSLPPQYS---GLDRI 289
QY 290 IHPVPAALTLDPGTAHORLLISDDCTIVAYGNLHPQLODSKPRFDEVSVLGSEAFSSG 349
DB 290 IKPFQVDVILDNTAHPQLLVSEDRKAVRYERKKRNICYD-PRRFYVCPAVLGSQRFSSG 348
QY 350 VHYVEVVVAEKTQWVIGLAHEAASRKGSIQIOPS--RGFYCIVMHDGNOYSACTEPWTRL 407
DB 349 RHYWEVEGNKPKWILGVQCDCLLR--NWQDQPSVLGGFWAIGRYMKSGYVASGPKTQL 406
QY 408 NVRDKLDKVGVDYDQGLLIYFNADMSWLTFFREKFFKLCYSFSPQOSHANGKNVQ 467
DB 407 LPWKPFSKIGIFLDYELGDLSPFNMDRSILYTFNDCFTFAVWPYF-----YTGTDSEP 460
QY 468 LRINTV 473
DB 461 LKICSV 466

RESULT 10
US-10-104-047-3664
Sequence 3664, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1el full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:

```

; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 3664
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3664

```

Query Match.	20.0%;	Score 500;	DB 15;	Length 468;
Best Local Similarity	27.5%;	Pred. No. 2.8e-33;		
Matches 133;	Conservative 91;	Mismatches 212;	Indels 48;	Gaps 11;
QY	4	SLKDELLCSYLSIYQDPVSLGCEHYECRCITTEHWVQEOAGQARDCEPCERTFAEPA	63	
Db	9	NLRKEULTFICLDYFSSFVTECHSFCVLCLLSW--EHNTPISCEPWRTLEGPHFQ	66	
QY	64	PSUKLANIVERYSSFPDAILNARRARPCQAHDKVLCITLDRALLCFQDEPA----	118	
Db	67	SNERLGR-----ASIAQLRSQVLQSEDEQSGYGRMPTTAKALSDDEQGSFAV	116	
QY	119	--LHEQHVGTIDDAFDELORELBKDLOALQDSREHTEALQLLKROLAETKSTKSLRT	176	
Db	117	AQGHGANKRVLSGEAEHREKLEQIILNLRVRKQAQVILTHEKERVKLCQEBTKCKQ	176	
QY	177	TIGEAPELRLRLRERKAMLEELADTARTLTIDIEQVQVYSQOLAKVQEGAILERL	236	
Db	177	VVSYENKMHQFLKEBEQLOQLLEQBEKENMRKLRNNEIKLTQOIRS-----LSKMI	229	
QY	237	AETDRHTFLAGVASLSERLKGKIHET-----NLTYEDFPTSKYTGPLYTIKWSLFQ	288	
Db	230	AQIESSSQSAFESL--EVRGALERSFPLLQCPAATTELSLCRTIG-----MKE	279	
QY	289	DIHPVPAALTDPGTAHQRIILSDCTIVAYGNLHPQLODSKPRFVDEVSVLGSEAPSS	348	
Db	280	MLRKFSITEITLDPATANAYLVLSDELKSVKYGSSR--QQLPDNPERFQDSATVLGTQIFTS	338	
QY	349	GVHYWVVAEKTQWIGLAEHAASRKGSIQIQPSRGFYCIVMHDGNQYSA--CTEPTWRL	407	
Db	339	GRHYWEVGVNKTWEVGVICKDSVSRKGNLPKPPGDLFSLIGLKIGDDYDLWVSSPLKQG	398	
QY	408	NVRDKLDKGVFDYDQGLLIFYNADMSWLYTF--REKFPFKLCSYFSPQOSHANGKNVQ	466	
Db	399	HVREPKGVGLDYSCHIAFNCTGIDTESLIYFPPQASFOEARLPITESCLPN--EGINTD	457	
QY	467	PLRI 470		
Db	458	PLTI 461		

```

RESULT 11
US-10-093-463-74
/ Sequence 74, Application US/10093463
/ Publication No. US200208039A1
/ GENERAL INFORMATION:
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Pochart, Pascal
/ APPLICANT: Zhong, Mei
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Mezes, Peter
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Casman, Stacie
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Li, Li
/ APPLICANT: Zetthusen, Bryan
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Vernet, Corinne

```

1	APPLICANT:	Pena, Carol
2	APPLICANT:	Burgess, Catherine
3	APPLICANT:	Liu, Xiaohong
4	APPLICANT:	Spytek, Kimberly
5	APPLICANT:	Gorman, Linda
6	APPLICANT:	Spaderna, Steven
7	APPLICANT:	Voss, Edward
8	APPLICANT:	Malyankar, Uriel
9	APPLICANT:	Anderson, David
10	APPLICANT:	Patturajan, Meera
11	APPLICANT:	Miller, Charles
12	APPLICANT:	Taupier, Raymond J. Jr.
13	TITLE OF INVENTION:	NO. US20030208039A1el
14	TITLE OF INVENTION:	Encoding The Antigen
15	FILE REFERENCE:	21402-290A (Cura 590AT)
16	CURRENT APPLICATION NUMBER:	US/10/093, 463
17	CURRENT FILING DATE:	2002-06-24
18	PRIOR APPLICATION NUMBER:	60/283, 675
19	PRIOR FILING DATE:	2001-04-14
20	PRIOR APPLICATION NUMBER:	60/338, 092
21	PRIOR FILING DATE:	2001-12-03
22	PRIOR APPLICATION NUMBER:	60/274, 281
23	PRIOR FILING DATE:	2001-03-08
24	PRIOR APPLICATION NUMBER:	60/274, 101
25	PRIOR FILING DATE:	2001-03-08
26	PRIOR APPLICATION NUMBER:	60/325, 681
27	PRIOR FILING DATE:	2001-09-27
28	PRIOR APPLICATION NUMBER:	60/304, 354
29	PRIOR FILING DATE:	2001-07-10
30	PRIOR APPLICATION NUMBER:	60/279, 995
31	PRIOR FILING DATE:	2001-03-30
32	PRIOR APPLICATION NUMBER:	60/294, 899
33	PRIOR FILING DATE:	2001-05-31
34	PRIOR APPLICATION NUMBER:	60/287, 424
35	PRIOR FILING DATE:	2001-04-30
36	PRIOR APPLICATION NUMBER:	60/299, 027
37	PRIOR FILING DATE:	2001-06-18
38	PRIOR APPLICATION NUMBER:	60/309, 198
39	PRIOR FILING DATE:	2001-07-31
40	PRIOR APPLICATION NUMBER:	60/281, 194
41	PRIOR FILING DATE:	2001-04-04
42	PRIOR APPLICATION NUMBER:	60/274, 194
43	PRIOR FILING DATE:	2001-03-08
44	PRIOR APPLICATION NUMBER:	60/274, 849
45	PRIOR FILING DATE:	2001-03-09
46	PRIOR APPLICATION NUMBER:	60/330, 380
47	PRIOR FILING DATE:	2001-10-18
48	PRIOR APPLICATION NUMBER:	60/275, 235
49	PRIOR FILING DATE:	2001-03-12
50	PRIOR APPLICATION NUMBER:	60/288, 342
51	PRIOR FILING DATE:	2001-05-03
52	PRIOR APPLICATION NUMBER:	60/275, 578
53	PRIOR FILING DATE:	2001-03-13
54	NUMBER OF SEQ ID NOS:	370
55	SOFTWARE:	PatentIn Ver. 2.1
56	SEQ ID NO 74	
57	LENGTH:	4675
58	TYPE:	PRT
59	ORGANISM:	Homo sapiens
60	US-10-093-463-74	

[illegible]

QY 61 ALAPSLKLANIVERYSFPLDAILNARRAARPCQAH-DKVKLFCLTDRLALLCFCCDEPAL 119
Db 70 SLRPNKQLGSLIE-----ALKETDQEMSCBEHGEQFHLFCDEGQLICWRCERAPQ 120
QY 120 HQHQVGTGDDAFDELQRELDQALQDSREHTEALQLLKRLQALAEKTSKSLRTTIG 179
Db 121 HKGHTTALVEDVCOGYKEKLEQAVTKLKQLEDRCCTEQKLSAMRITTKWKEKVQIQORQKIR 180
QY 180 EAFERLHRLREROKAMLELEADTARTLT---DIEQKVQVYSQOLR-----KVQEG 228
Db 181 SDFXNLQCFHHEEKSVYLRLEKEEQOTLSRLRDYEAGLGLKSNELKSHILEEKCQGS 240
QY 229 AQILQERLAETDRHTFLAGVASLSRLKGIHETNLTYDEPFTSKYTGPLQYTIWKSIFQ 288
Db 241 AQKLLQNVNDT-----LSRSWAVKLETSEAVSLELHMTCNVSKLYFDVKMLRS 289
QY 289 DIHPVPAALTDPGTAHQRLILSDCTIVAYGNLHPQLQD-SPKRFDEVSVLGSEAFS 347
Db 290 --HQV--SVTLDPDTAHHELILSEDRROVTRG--YTQENQDTSRRRFTAFPCVLGCEGFT 343
QY 348 SGVHYWEVVVAEKTQWVIGLAHEAASRKSGSIQIPSRGFCYCIVMHDMGNQYSACTEPWTRL 407
Db 344 SGRRYFEVDVGEGTGMDLGVCMENVRQGTGMKQEPQSGFWTLRLCKKGYVALTSPPTSL 403
QY 408 NVRKLDKVGVELDYDQGLLIFYNADMSWLYTF-REKFPKGKLCYSF 453
Db 404 HLHQPLLGVFLDYEAGVSVFYNGTGTCHFTFPKASFSDTLRPF 450

RESULT 14

US-10-617-217A-97
; Sequence 97, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-97

Query Match 19.6%; Score 492; DB 16; Length 465;
Best Local Similarity 29.3%; Pred. No. 1.3e-32;
Matches 137; Conservative 80; Mismatches 206; Indels 44; Gaps 11;
QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWRQEAQAGD-----CPECRTFAEP 60
Db 10 MMEATATCSICLSLMTNPVINCCHSYCHLCITDFFKNPSQKQLRQETFTCCPQCRAPFHM 69
QY 61 ALAPSLKLANIVERYSFPLDAILNARRAARPCQAH-DKVKLFCLTDRLALLCFCCDEPAL 119
Db 70 SLRPNKQLGSLIE-----ALKETDQEMSCBEHGEQFHLFCDEGQLICWRCERAPQ 120
QY 120 HQHQVGTGDDAFDELQRELDQALQDSREHTEALQLLKRLQALAEKTSKSLRTTIG 179

Db 121 HKGHTTALVEDVCOGYKEKLEQAVTKLKQLEDRCCTEQKLSAMRITTKWKEKVQIQORQKIR 180
QY 180 EAFERLHRLREROKAMLELEADTARTLT---DIEQKVQVYSQOLR-----KVQEG 228
Db 181 SDFXNLQCFHHEEKSVYLRLEKEEQOTLSRLRDYEAGLGLKSNELKSHILEEKCQGS 240
QY 229 AQILQERLAETDRHTFLAGVASLSRLKGIHETNLTYDEPFTSKYTGPLQYTIWKSIFQ 288
Db 241 AQKLLQNVNDT-----LSRSWAVKLETSEAVSLELHMTCNVSKLYFDVKMLRS 289
QY 289 DIHPVPAALTDPGTAHQRLILSDCTIVAYGNLHPQLQD-SPKRFDEVSVLGSEAFS 347
Db 290 --HQV--SVTLDPDTAHHELILSEDRROVTRG--YTQENQDTSRRRFTAFPCVLGCEGFT 343
QY 348 SGVHYWEVVVAEKTQWVIGLAHEAASRKSGSIQIPSRGFCYCIVMHDMGNQYSACTEPWTRL 407
Db 344 SGRRYFEVDVGEGTGMDLGVCMENVRQGTGMKQEPQSGFWTLRLCKKGYVALTSPPTSL 403
QY 408 NVRKLDKVGVELDYDQGLLIFYNADMSWLYTF-REKFPKGKLCYSF 453
Db 404 HLHQPLLGVFLDYEAGVSVFYNGTGTCHFTFPKASFSDTLRPF 450

RESULT 15

US-10-024-298A-99
; Sequence 99, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-99

Query Match 19.5%; Score 489; DB 14; Length 465;
Best Local Similarity 29.3%; Pred. No. 2.3e-32;
Matches 137; Conservative 79; Mismatches 207; Indels 44; Gaps 11;
QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWRQEAQAGD-----CPECRTFAEP 60
Db 10 MMEATATCSICLSLMTNPVINCCHSYCHLCITDFFKNPSQKQLRQETFTCCPQCRAPFHM 69
QY 61 ALAPSLKLANIVERYSFPLDAILNARRAARPCQAH-DKVKLFCLTDRLALLCFCCDEPAL 119
Db 70 SLRPNKQLGSLIE-----ALKETDQEMSCBEHGEQFHLFCDEGQLICWRCERAPQ 120
QY 120 HQHQVGTGDDAFDELQRELDQALQDSREHTEALQLLKRLQALAEKTSKSLRTTIG 179
Db 121 HKGHTTALVEDVCOGYKEKLEQAVTKLKQLEDRCCTEQKLSAMRITTKWKEKVQIQORQKIR 180

```
QY 180 EAFERLHRLREROKAMLELEADTARTLT--DIEQVQVYSQQLR-----KVQEG 228
Db 181 SDFANLOCFLHBEKSYLWLEKEEQTLKRLRDEYAGLGKSNELKSHILELEKCGS 240
QY 229 AQIIQERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDFPPTSXYTGPLOYTIWKSLEFQ 288
Db 241 AQKLLQNVNT-----LSRSWAVKLETSEAVSLEHTMCNVSKLYFDVKMLRS 289
QY 289 DIHPVPAALTLDPGTAHORLILSDDCITIVAYGNLHPQLQD-SPKRFDFVEVSVLGSEAFS 347
Db 290 --HQV--SVTLDPDTAHHELILSDDRQVTRG--YTOENQDTSRRRFTAFPCVLGCEGFT 343
QY 348 SGVHYWEVVAEKTQWIGLAHEAASRKSGIQIOPSRGFYCIVMHDCNQXSACTEPWTRL 407
Db 344 SGRRYFEDVGEGTGWDLGVCMENVRGTGMKQEPQSGFWTLRLCKKKGYVALTSPPTSL 403
QY 408 NVRDKLKVGVFLDYDQGLLIFYNADDMSWLYTF-REKFPGLCSYF 453
Db 404 HLHEQPLLVGIFLDYEAGVVSFYNGNTCCHIFTFPKASFSDTLRPYF 450
```

Search completed: July 23, 2004, 15:13:46
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:03:00 ; Search time 55 Seconds
(without alignments)
2440.183 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELICLSIYQD.....GQSHANGKNVQPLRINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2504	100.0	475	5 AAU78657	AAU78657 Human tum
2	2504	100.0	475	7 ADC37269	ADC37269 Nuclear f
3	2491	99.5	475	4 AAB93138	AAB93138 Human pro
4	1983	79.2	394	7 ADC37455	ADC37455 Nuclear f
5	1312	52.4	304	5 AAU78658	AAU78658 Human tum
6	662.5	26.5	488	7 ADC37445	ADC37445 Nuclear f
7	634	25.3	123	4 AAM88857	AAM88857 Human imm
8	631	25.2	735	4 ABG26213	ABG26213 Novel hum
9	613	24.5	500	4 AAG89346	AAG89346 Human sec
10	583	23.3	513	7 ADC37447	ADC37447 Nuclear f
11	583	23.3	580	3 AAB43498	AAB43498 Human can
12	567	22.6	486	6 ABJ38678	ABJ38678 Human nuc
13	560	22.4	468	5 ABG97352	ABG97352 Human CGD
14	552.5	22.1	475	2 AAR15148	AAR15148 Ro/SSA au
15	550.5	22.0	485	5 AAM48396	AAM48396 Human SSA
16	550.5	22.0	485	5 ABP64866	ABP64866 Human pro
17	550.5	22.0	485	6 ABP55392	ABP55392 Human MDD
18	550.5	22.0	511	7 ADC37443	ADC37443 Nuclear f
19	541.5	21.6	485	6 ADA55047	ADA55047 Human pro
20	520	20.8	516	4 AAE02616	AAE02616 Murine ha
21	505.5	20.2	488	4 AAB95331	AAB95331 Human pro
22	501	20.0	471	7 ADB65328	ADB65328 Human pro
23	500	20.0	468	7 ADB65510	ADB65510 Human pro
24	499.5	19.9	4675	5 ABP70085	ABP70085 Human NOV
25	492	19.6	465	5 ABP61472	ABP61472 Human NF-

26	491	19.6	630	7	ADC37237	ADC37237 Nuclear f
27	489	19.5	465	2	AAW78921	AAW78921 Human hae
28	489	19.5	465	5	ABP61473	ABP61473 Human NF-
29	487	19.4	717	4	ABG21361	ABG21361 Novel hum
30	483	19.3	493	4	AAE02618	AAE02618 Human hae
31	483	19.3	504	4	AAE02617	AAE02617 Human hae
32	475.5	19.0	4691	5	ABP70084	ABP70084 Human NOV
33	458	18.3	477	3	AAB42919	AAB42919 Human ORF
34	449	17.9	539	6	ABU03730	ABU03730 Human exp
35	449	17.9	539	6	ABU03731	ABU03731 Human exp
36	449	17.9	539	6	ABU03729	ABU03729 Human exp
37	449	17.9	539	6	ABU03732	ABU03732 Human exp
38	438.5	17.5	545	7	ADC37235	ADC37235 Nuclear f
39	433.5	17.3	781	2	AAU09001	AAU09001 FMF assoc
40	427.5	17.1	781	5	AAO17853	AAO17853 Pryn dom
41	422.5	16.9	477	2	AAU01522	AAU01522 Human mar
42	418	16.7	475	3	AAAB29655	AAAB29655 Human mem
43	418	16.7	475	5	ABG79337	ABG79337 Human foe
44	418	16.7	475	6	ADA54825	ADA54825 Human pro
45	414.5	16.6	488	4	ABB50231	ABB50231 Human tra

ALIGNMENTS

RESULT 1

AAU78657
ID AAU78657 standard; protein; 475 AA.

XX AC AAU78657;

XX DT 18-JUN-2002 (first entry)

XX DE Human tumour suppressor CAR-1.

XX KW Human; tumour suppressor; CAR-1; cytostatic; cancer; tumour;

KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;

KW colon cancer; stomach cancer; breast cancer; endometrial cancer;

KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;

KW head and neck cancer; oesophageal cancer; bone marrow cancer;

XX chromosome lp31-1p36.

XX OS Homo sapiens.

XX EN WO200212285-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US025269.

XX PR 10-AUG-2000; 2000US-0225033P.

XX PR 23-AUG-2000; 2000US-0227560P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Killary A, Chandler D, Lott S;

XX DR WPI; 2002-269088/31.

XX DR N-PSDB; ABK12806.

XX PT New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for

PT diagnosing cancer, for altering the phenotype of a tumor cell, for

XX treating cancers or as a diagnostic or prognostic indicator of cancer.

XX Claim 23; Page 131-132; 185pp; English.

XX The invention relates to an isolated polynucleotide encoding a

CC polypeptide being tumour suppressor, CAR-1. Also included are fragments

CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein

CC from 10-50 amino acids, an expression cassette comprising the

CC polynucleotide under the control of a promoter operable in eukaryotic

CC cells, a method for suppressing growth of a cancer cells by contacting

CC the cells with the expression cassette (i.e. gene therapy), a cell

CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody, a hybridoma cell that produces the monoclonal
 CC antibody, a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1, or by
 CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC non-transgenic eukaryote, a method of screening a candidate substance for
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
 CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
 CC altering the phenotype of a tumour cell, for treating cancers (e.g.
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
 CC other tissues), and as a diagnostic or prognostic indicator of cancer.
 CC CAR-1 may also be used in screening compounds for activity in either
 CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
 CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
 CC chromosome 1 (1p31-1p36). The present sequence represents human CAR-1
 CC
 XX
 SQ Sequence 475 AA;

Query Match 100.0%; Score 2504; DB 5; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.3e-208;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 Db 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 QY 61 ALAPSLKLANIVERYSSFPDLALINARRAAPCOAHDKVKLFCLTDRLALCFCDPEPALH 120
 Db 61 ALAPSLKLANIVERYSSFPDLALINARRAAPCOAHDKVKLFCLTDRLALCFCDPEPALH 120
 QY 121 EQHVTGIDDAFDELQRELKDQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 Db 121 EQHVTGIDDAFDELQRELKDQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 QY 181 APERHLRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVOEGAQILQERLAETD 240
 Db 181 APERHLRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVOEGAQILQERLAETD 240
 QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDHPVPAALTLD 300
 Db 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDHPVPAALTLD 300
 QY 301 PGTAHORLLSDCTTIVAGNLHPQLQDSPKRFDEVSILGSEAFSSGVHYVEVVAAEK 360
 Db 301 PGTAHORLLSDCTTIVAGNLHPQLQDSPKRFDEVSILGSEAFSSGVHYVEVVAAEK 360
 QY 361 TQWVIGLAHEAARSGKSIQIOPSRGFYCIWMHGNQYSACTEPWTRLNVRDKLDKGVFL 420
 Db 361 TQWVIGLAHEAARSGKSIQIOPSRGFYCIWMHGNQYSACTEPWTRLNVRDKLDKGVFL 420
 QY 421 DYDQGLLIIFYNADMSWLYTFREKFPKGLCSYFSPGSHANGKNVQPLRINTVRI 475
 Db 421 DYDQGLLIIFYNADMSWLYTFREKFPKGLCSYFSPGSHANGKNVQPLRINTVRI 475

RESULT 2
 ADC37269
 ID ADC37269 standard; protein; 475 AA.

XX ADC37269;
 AC 18-DEC-2003 (first entry)
 DT Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 102.
 DE Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antinflammatory;
 KW immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 XX Homo sapiens.
 OS
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 XX 03-DEC-2002; 2002WO-JP012644.
 XX
 XX 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 XX (ASAH) ASAH KASEI KK.
 PA
 XX Matsuda A, Muramatsu S;
 PI WPI; 2003-505282/47.
 XX
 DR N-PSDB; ADC37268.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 useful for treating inflammation, autoimmune diseases, cancers, or
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 PS Claim 1; SEQ ID NO 102; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 SQ Sequence 475 AA;
 Query Match 100.0%; Score 2504; DB 7; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.3e-208;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 Db 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 QY 61 ALAPSLKLANIVERYSSFPDLALINARRAAPCOAHDKVKLFCLTDRLALCFCDPEPALH 120
 Db 61 ALAPSLKLANIVERYSSFPDLALINARRAAPCOAHDKVKLFCLTDRLALCFCDPEPALH 120
 QY 121 EQHVTGIDDAFDELQRELKDQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 Db 121 EQHVTGIDDAFDELQRELKDQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 QY 181 APERHLRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVOEGAQILQERLAETD 240
 Db 181 APERHLRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVOEGAQILQERLAETD 240
 QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDHPVPAALTLD 300
 Db 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDHPVPAALTLD 300

QY 301 PCTAHQRLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWVVVAEK 360
DB 301 PCTAHQRLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWVVVAEK 360
QY 361 TQWVIGLAHEAASRKSGSIQIOPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
DB 361 TQWVIGLAHEAASRKSGSIQIOPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
QY 421 DYDQGLLIFYNADDMWSLTYTFRKFPKGLCSYFSPGQSHANGKNVQPLRINTVRI 475
DB 421 DYDQGLLIFYNADDMWSLTYTFRKFPKGLCSYFSPGQSHANGKNVQPLRINTVRI 475

RESULT 3
ID AAB93138 standard; protein; 475 AA.
AC AAB93138;
XX
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:12037.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
XX
XX 27-AUG-1999; 99JP-00300253.
XX
XX 11-JAN-2000; 2000JP-00118776.
XX
XX 02-MAY-2000; 2000JP-00183767.
XX
XX 09-JUN-2000; 2000JP-00241899.
XX
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 8; SEQ ID NO 12037; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent

CC oligonucleotides, all of which are used in the exemplification of the present invention
XX
SQ Sequence 475 AA;
Query Match 99.5%; Score 2491; DB 4; Length 475;
Best Local Similarity 99.6%; Pred. No. 3.1e-207;
Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MACSLDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQBAQAGDCECRRTEAEP 60
DB 1 MACSLDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQBAQAGDCECRRTEAEP 60
QY 61 ALAPSLKLANIVERYSSFFLDAILNARRARPCQAHDKVLCITDREALICFCDDEPALH 120
DB 61 ALAPSLKLANIVERYSSFFLDAILNARRARPCQAHDKVLCITDREALICFCDDEPALH 120
QY 121 EQHOVTGIDDAFDELQRELKDQALQDSREHTEALQILKROLAETKSKSLRTTIGE 180
DB 121 EQHOVTGIDDAFDELQRELKDQALQDSREHTEALQILKROLAETKSKSLRTTIGE 180
QY 181 AFERLHRLLEERQKAMLELEADTARTLTIDIEOKVQRYSOQLRKVOEGAQILQRLAETD 240
DB 181 AFERLHRLLEERQKAMLELEADTARTLTIDIEOKVQRYSOQLRKVOEGAQILQRLAETD 240
QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDFTSKYTGLOVYTIWKSIFQDTHPVPAALTLD 300
DB 241 RHTFLAGVASLSERLKGKIHETNLTYEDFTSKYTGLOVYTIWKSIFQDTHPVPAALTLD 300
QY 301 PGTAHQRLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWVVVAEK 360
DB 301 PGTAHQRLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWVVVAEK 360
QY 361 TQWVIGLAHEAASRKSGSIQIOPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
DB 361 TQWVIGLAHEAASRKSGSIQIOPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
QY 421 DYDQGLLIFYNADDMWSLTYTFRKFPKGLCSYFSPGQSHANGKNVQPLRINTVRI 475
DB 421 DYDQGLLIFYNADDMWSLTYTFRKFPKGLCSYFSPGQSHANGKNVQPLRINTVRI 475

RESULT 4
ADC37455
ID ADC37455 standard; protein; 394 AA.
XX
XX ADC37455;
XX
XX 18-DEC-2003 (first entry)
XX
XX Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 288.
XX
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease; cancer; infectious disease; bone disease; AIDS;
XX
XX neurodegenerative disease; ischaemic disorder; Antiinflammatory;
XX
XX Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
XX
XX Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2003048202-A2.
XX
XX 12-JUN-2003.
XX
XX 03-DEC-2002; 2002WO-JP012644.
XX
XX 03-DEC-2001; 2001JP-00368692.
XX
XX 05-DEC-2001; 2001US-0335829P.
XX
XX 03-OCT-2002; 2002JP-00291302.
XX
XX 04-OCT-2002; 2002US-0415769P.
XX
XX (ASAH) ASAH KASEI KK.
XX


```
PI Matsuda A, Muramatsu S;
XX
DR WPI; 2003-505282/47.
XX N-PSDB; ADC37454.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
PS Claim 1; SEQ ID NO 288; 938pp; English.
XX
XX The present invention relates to novel proteins and their coding
XX sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
XX kappaB). The proteins and their coding sequences are useful for treating
XX a disease associated with NF-kappaB activation, such as inflammation,
XX autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
XX neurodegenerative diseases, or ischaemic disorders.
XX
SQ Sequence 394 AA;
Query Match 79.2%; Score 1983; DB 7; Length 394;
Best Local Similarity 100.0%; Pred. No. 3e-163;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
Db 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
Oy 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCCQAHDKVKLFCLTDRALLCFFCDEPALH 120
Db 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCCQAHDKVKLFCLTDRALLCFFCDEPALH 120
Oy 121 EQHQTGIDDAFDELQRELKQQLQALQDSREHTEALQKQLAETKSKSLTTTIGE 180
Db 121 EQHQTGIDDAFDELQRELKQQLQALQDSREHTEALQKQLAETKSKSLTTTIGE 180
Oy 181 APERLHRLLREROKAMLELEADTARTLTDIEQVQRYSQQLRVQEGAILQERLAETD 240
Db 181 APERLHRLLREROKAMLELEADTARTLTDIEQVQRYSQQLRVQEGAILQERLAETD 240
Oy 241 RHTFLAGVASLSERLKGKHETNLTYEDFPTSKYTGPLQYTIWKSFLQDIIHPVPAALTLD 300
Db 241 RHTFLAGVASLSERLKGKHETNLTYEDFPTSKYTGPLQYTIWKSFLQDIIHPVPAALTLD 300
Oy 301 PCTAHORLILSDDCITIVAYGNLHPQLODSPKRFDEVEVSLGSEAFSSGVHYWEVVAEK 360
Db 301 PCTAHORLILSDDCITIVAYGNLHPQLODSPKRFDEVEVSLGSEAFSSGVHYWEVVAEK 360
Oy 361 TQWVIGLAHEAASRKGSIIQI 381
Db 361 TQWVIGLAHEAASRKGSIIQI 381
RESULT 5
AAU78658
ID AAU78658 standard; protein; 304 AA.
AC AAU78658;
XX
XX 18-JUN-2002 (first entry)
XX
XX Human tumour suppressor CAR-1 produced by alternative splicing.
XX
XX Human; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
XX gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
XX colon cancer; stomach cancer; breast cancer; endometrial cancer;
XX prostate cancer; testicular cancer; ovarian cancer; skin cancer;
XX head and neck cancer; oesophageal cancer; bone marrow cancer;
XX chromosome 1p31-1p36.
XX
XX Homo sapiens.
XX
XX
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PN WO200212285-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025269.
XX
XX 10-AUG-2000; 2000US-0225033p.
XX
XX 23-AUG-2000; 2000US-0227560p.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Killary A, Chandler D, Lott S;
XX
XX WPI; 2002-269088/31.
XX
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
XX diagnosing cancer, for altering the phenotype of a tumor cell, for
XX treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
XX Claim 23; Page 133; 185pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
XX polypeptide being tumour suppressor, CAR-1. Also included are fragments
XX of the polynucleotide from 15-5000 nucleotides, fragments of the protein
XX from 10-50 amino acids, an expression cassette comprising the
XX polynucleotide under the control of a promoter operable in eukaryotic
XX cells, a method for suppressing growth of a cancer cells by contacting
XX the cells with the expression cassette (i.e. gene therapy), a cell
XX comprising the expression cassette, an anti-CAR-1 monoclonal or
XX polyclonal antibody, a hybridoma cell that produces the monoclonal
XX antibody, a method of diagnosing a cancer by assessing the expression of
XX CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
XX methods for altering the phenotype of a tumour cell, methods for treating
XX a subject with cancer by administering the tumour suppressor CAR-1, or by
XX administering a nucleic acid encoding the tumour suppressor CAR-1 and a
XX promoter active in eukaryotic cells, where the promoter is operably
XX linked to the region encoding the tumour suppressor, a non-human
XX transgenic eukaryote lacking a functional CAR-1 gene, a non-human
XX transgenic eukaryote that over-expresses CAR-1 as compared to a similar
XX non-transgenic eukaryote, a method of screening a candidate substance for
XX anti-tumour activity by contacting a cell lacking functional CAR-1
XX polypeptide, with a candidate substance and determining the effect of the
XX candidate substance on the cell, an anti-tumour composition produced by
XX contacting a cell lacking functional CAR-1 polypeptide, with a candidate
XX substance, determining the effect of the candidate substance on the cell,
XX identifying a candidate inhibitor substance, and making a composition and
XX an isolated and purified nucleic acid that hybridizes, under high
XX stringency conditions, to a DNA segment comprising about 15-3826 bases of
XX the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
XX altering the phenotype of a tumour cell, for treating cancers (e.g.
XX cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
XX intestine, blood cells, colon, stomach, breast, endometrium, prostate,
XX testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
XX other tissues), and as a diagnostic or prognostic indicator of cancer.
XX CAR-1 may also be used in screening compounds for activity in either
XX stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
XX effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
XX chromosome 1 (1p31-1p36). The present sequence represents a variant human
XX CAR-1 produced by alternative splicing of the CAR-1 cDNA
XX
XX Sequence 304 AA;
Query Match 52.4%; Score 1312; DB 5; Length 304;
Best Local Similarity 91.8%; Pred. No. 3.8e-105;
Matches 257; Conservative 2; Mismatches 5; Indels 16; Gaps 1;
Oy 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
Db 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
Oy 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCCQAHDKVKLFCLTDRALLCFFCDEPALH 120
Db 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCCQAHDKVKLFCLTDRALLCFFCDEPALH 120
```

QY 121 EQHVTGIDDAFDELQRELKDQALQDSREHTEALQLLKRLAETKSKSLRTTIGE 180
 Db 121 EQHVTGIDDAFDELQRELKDQALQDSREHTEALQLLKRLAETKSKSLRTTIGE 180
 QY 181 APERLHRLREROKAMLELEADTARTLTDIEQKVORYSQOLRVQVGAQILOERLAETD 240
 Db 181 APERLHRLREROKAMLELEADTARTLTDIEQKVORYSQOLRVQVGAQILOERLAETD 240
 QY 241 RHTFLAGVASLSRELK-----GKIHTNL 264
 Db 241 RHTFLAGVASLSERASRPNPGHSPDPVGRLLHCHGL 280

RESULT 6
 ADC37445
 ID ADC37445 standard; protein; 488 AA.
 AC ADC37445;
 XX
 DT 18-DEC-2003 (first entry)
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 278.
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS; Antiinflammatory;
 KW neurodegenerative disease; ischaemic disorder; Antimicrobial; Anti-HIV;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Gene therapy; human.
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 XX Homo sapiens.
 OS
 XX
 FN W02003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PE 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 XX (ASAH) ASAH KASEI KK.
 PA
 XX
 XX Matsuda A, Muramatsu S;
 PI
 XX
 DR WPI; 2003-505282/47.
 DR N-PSDB; ADC37444.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 XX Claim 1; SEQ ID NO 278; 938pp; English.
 PS
 XX The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX

Query Match 26.5%; Score 662.5; DB 7; Length 488;
 Best Local Similarity 33.2%; Pred. No. 1.9e-48;
 Matches 165; Conservative 79; Mismatches 186; Indels 67; Gaps 12;

QY 4 SLKDELLCSICLSIYDQVSLGCEHYFCRRICITEHWVRQEAQAGD--CPCEKRTFAEPA 61
 Db 22 NLQVEASVCLEVKELPEVIECGHNFCKACITRWEDLE----RDFPCPCVKRTSYRS 77

QY 62 LARSLKIANIVERYSSFPDLAIINARRARPC-QAHDKVKLFLCTDRALLCFDDEPALH 120
 Db 78 LRNRQLGSMVE--IAQLQAVRKIRDESLCPQHHEALSLFCYEDQEAVALCAISHTH 135
 QY 121 EQHVTGIDDAFDELQRELKDQALQDSREHTEALQLLKRLAETKSKSLRTTIGE 180
 Db 136 RAHTVVPDDATQYKELQKCLEPLEQKLEITRCKSSSEKPGELKRLVSRROQILR 195
 QY 181 APERLHRLREROKAMLELEADTARTLTDIEQKVORYSQOLRVQVGAQILOERLAETD 240
 Db 196 EFEEHLHRLDEEQVLLSLREEE-----EQDI-----LQRLRENAALGDKRRD-- 239
 QY 241 RHTFLAGVASLSRELKCK-----IHEINLTIVEDFTSKYTG-----P 277
 Db 240 -----LAHLAAVEGKCLQSGFEMLKDKVCKEKEKVKMTVEVTSVSELEKNFNFP 292
 QY 278 LQY----TIWKSILFQDIHPVPAALTLDPGTAHQRLILSDCTIVAYGNLHPQPLQDSPKR 333
 Db 293 RQYFALEKILKLIADV-----TLDPEAHNLVLSEDRKSVKVFETRLDLPDTPRR 345
 QY 334 FDEVSVLGSFAFSSGVHYWVVAEKTQWVIGLAHEAASRKSGSIQIPSRGFGYCVIMHD 393
 Db 346 FTFVPCVLATEGFTSGRHYWEVEVGDKTHWAVGVCRDSVSRKGLTLPETGYWRVRLWN 405
 QY 394 GNOYSACTEPWTRNLNVRDKLDKGVFLDYDQGLLI FYNADDMSLYTRFEKFPKLCYSF 453
 Db 406 GDKYAATTTPTPLHVKPKRVGIFLDYEAGTLSFYNVVTRSHIYFTDTFTFEKLMPLF 465
 QY 454 SPGQSHANGKNVQPLRI 470
 Db 466 YFG-IRAGRKNAAPLTI 481

RESULT 7
 AAM88857
 ID AAM88857 standard; protein; 123 AA.
 XX
 AC AAM88857;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen SEQ ID NO:16450.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX
 OS Homo sapiens.
 PN W0200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001354.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205151P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214686P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.

CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 123 AA;
Query Match 25.3%; Score 634; DB 4; Length 123;
Best Local Similarity 96.7%; Pred. No. 7.2e-47;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 288 QDIHPVPAALTLDPGTAHQRLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFS 347
Db 3 RDPFVPAALTLDPGTAHQRLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFS 62
QY 348 SGVHYWEVVAEKTQWVIGLAHEAASRKGSIQIOPSRGFCYIVMHDGNOYSACTEPTRL 407
Db 63 SGVHYWEVVAEKTQWVIGLAHEAASRKGSIQIOPSRGFCYIVMHDGNOYSACTEPWTRX 122
QY 408 N 408
Db 123 N 123
RESULT 8
ABG26213
ID ABG26213 standard; protein; 735 AA.
XX
AC ABG26213;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26204.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSR-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS90400.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 56572; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 735 AA;
Query Match 25.2%; Score 631; DB 4; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 168 KSSTKSLLRTTIGEAFERLHRLRRERQKAMLEELFADTARTLTDIEQVRSQQLRKVQE 227
Db 598 KSSTKSLLRTTIGEAFERLHRLRRERQKAMLEELFADTARTLTDIEQVRSQQLRKVQE 657
QY 228 GAQILQERLAETDRHTFLAGVASLSERLKGKIHTNLTYYEDPPTSKYTGPIQYTIWKSLE 287
Db 658 GAQILQERLAETDRHTFLAGVASLSERLKGKIHTNLTYYEDPPTSKYTGPIQYTIWKSLE 717
QY 288 QDIHP 292
Db 718 QDIHP 722
RESULT 9
AAG89346
ID AAG89346 standard; protein; 500 AA.
XX
AC AAG89346;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 466.
XX
KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET.
XX
OS Homo sapiens.
XX
PN WO200142451-A2.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-IB001938.
XX
PR 08-DEC-1999; 99US-0169629P.
PR 06-MAR-2000; 2000US-0187470P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX
DR WPI; 2001-367870/38.
DR N-PSDB; AAG64949.
XX
PT Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
PT diseases, and for diagnosis of those diseases.
XX
PS Claim 21; Page 913-914; 921pp; English.
XX
CC The invention relates to full length GENSET human nucleic acids encoding
CC potentially secreted proteins. The nucleic acids and the polypeptides
CC they encode may be used in the prevention, treatment and diagnosis of
CC diseases associated with inappropriate GENSET gene expression. For
CC example, they be used to treat disorders associated with decreased
CC gene expression by rectifying mutations or deletions in a patient's
CC genome that affect the activity of GENSET or by supplementing the
CC patients own production of GENSET polypeptides. Conversely, antisense

XX	AAB43498;
AC	08-FEB-2001 (first entry)
CC	Human cancer associated protein sequence SEQ ID NO:943.
DE	Human; cancer associated gene; cancer antigen; detection; cancer;
XX	diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
XX	antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
XX	antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
KW	dermatological; neuroprotective; thrombolytic; coagulant; neoplastic;
KW	vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW	allergic reaction; graft versus host disease; organ rejection;
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;
KW	neurological disease; drug screening.
XX	Homo sapiens.
OS	WO200053350-A1.
XX	21-SEP-2000.
PN	08-MAR-2000; 2000WO-US005882.
PD	12-MAR-1999; 99US-0124270P.
PP	(HUMA-) HUMAN GENOME SCI INC.
XX	Rosen CA, Ruben SM;
PI	WPI; 2000-587533/55.
XX	N-PSDB; AAC77707.
DR	Novel isolated nucleic acids comprising sequences encoding peptides
PT	useful for treating or diagnosing e.g. cancer.
PT	Claim 11; Page 1506-1508; 2352pp; English.
PS	AAC77607 to AAC78448 encode the human cancer associated proteins given in
XX	AAB43398 to AAB44239. The proteins can have activities based on the
CC	tissues and cells the genes are expressed in. Example of activities
CC	include: cytostatic; proliferative; vulnerable; immunomodulator;
CC	antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC	antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC	dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC	neotrophic; vasotropic; antipsoriatic and angiogenic. The
CC	polynucleotides and polypeptides can be used for preventing, treating or
CC	ameliorating medical conditions and diagnosing pathological conditions.
CC	Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC	the present invention may be used to treat immune disorders by activating
CC	or inhibiting the proliferation, differentiation or mobilisation of
CC	immune cells, to treat disorders of haematopoietic cells, autoimmune
CC	disorders, allergic reactions, graft versus host disease and organ
CC	rejection, modulate haemostatic or thrombolytic activity, modulate
CC	inflammation, cancers, cardiovascular disorders, neurological disease and
CC	bacterial or viral infections. The peptides, nucleotides, antibodies,
CC	agonists and antagonists may be also be used in drug screens. AAC78449 to
CC	AAC78457 and AAB44240 represent sequences used in the exemplification of
CC	the present invention
XX	Sequence 580 AA;
SQ	Query Match 23.3%; Score 583; DB 3; Length 580;
	Best Local Similarity 29.1%; Pred.No.2e-41;
	Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;
QY	5 LKDELCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAGGRDCPCERTFAEPALAP 64
Db	77 LQOETTCPCVLQVFAPPEMLDSCGHNICCAILARCWGTAETNVIS--CPQCRFTFFQRHMRF 134
QY	65 SLKLAINVERYSFPFLDALINARRAARP-----COAH-DKVKLFCLTDRALLCFCF 114

DR WPI; 2003-248084/24.
DR N-PSDB; AB242527.
XX
PT New human nucleic acid associated proteins (NAAP), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
PT infections.
XX
XX Claim 1; Page 197-198; 263pp; English.
XX
XX The invention comprises the amino acid and coding sequences of human
XX nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
XX the invention are useful for diagnosing, treating and preventing diseases
XX or conditions associated with the decreased expression or overexpression
XX of NAAP, such as: cell proliferative disorders (e.g. cancer);
XX neurological disorders (e.g. epilepsy); immune/inflammatory disorders
XX (e.g. AIDS and allergies); and developmental disorders (e.g. Cushing's
XX syndrome). The present amino acid sequence represents a human nucleic
XX acid-associated protein of the invention
XX
XX Sequence 486 AA;
XX
Query Match 22.6%; Score 567; DB 6; Length 486;
Best Local Similarity 31.6%; Pred. No. 3.8e-40;
Matches 149; Conservative 73; Mismatches 194; Indels 56; Gaps 13;
QY 5 LKDELLCSICLSIYQDPVSLGCHVFCRCITEHWVROE-AQ-GARDQCECHRTFAEPAL 62
DB 10 LREDARCFVCLDFLOEPVSVDCGH3FCFLRCISEFCSEKSDGAGGVYACPCRCGRPFPSGF 69
QY 63 APSKLANIVYRSFPLDALINARARPCQAH-DKVKLFCLTDRALICFFCDPEPALHE 121
DB 70 RENROLGLVSVRRILGLGAGPCARCAR----HGEDLSRFCEDEALCWCDAGPEHR 125
QY 122 QHQVTGIDDAFDELORELKQALQDSREHEALQLKRLQ--AETKSKTSKSLRTTIG 179
DB 126 THRTAPLQEAAGSYQVKLQ-----MALELMRKELEDALTOEANVGKKTIV 171
QY 180 E-----AFERHRLREROKAMLELEADTARTLTDISQKVORYSQQLKVOE 227
DB 172 KEKVENQORFRLEFEKRGFLAQEQORLRLEAEERATLQRLRESKSLVQSQKALKE 231
QY 228 GAQIQERLAE'DRHTFTAGVASLSRLGKHINLTVEDPPTSXYTG---PQVYTIWK 284
DB 232 LADELQER-CQPALGLLGVSGVLSRSKA---VTRLEANNIPMELKTCACPIGRRELLR 287
QY 285 SLFQDIHPVPAALUTDPGTAHQRLILSDCTTIVAYGNLHPQLQD---SPKRPDVEVSYL 341
DB 288 KFQVDV-----KLDPAATHPSLLLTADLSRVQDG---EPWRDVPNNPFRFTWPCIL 336
QY 342 GSEAFSSGVHYVEVVAEYKTQWVIGLAHEAARSGSIQIOPSRGFYCIWHDGNQYSACT 401
DB 337 GLQSFSSGHEHYVEVLVGEAGWGLGVCQDTLPKGBTTPSPNGVWALWLLKGNMYMLA 396
QY 402 EBPWTRINVRDKLVGVLDYDQGLLIFYNADMSWLYTFREKFPCKLGSYF 453
DB 397 SFSVPLQLLESRCIGIFLDYERAGEISFNTVDGSIYITFNQLPSGLLRPYF 448
RESULT 13
ID ABG97352
XX ABG97352 standard; protein; 468 AA.
AC ABG97352;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human CGDD3, INCYTE 3089944CD1.
XX
XX Human; cell growth, differentiation; death; CGDD; cancer;
KW cell proliferative disorder; atherosclerosis; atherosclerosis;
KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;
KW polycythaemia vera; primary thrombocytopaenia; developmental disorder;

KW renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;
KW neurological disorder; Alzheimer disease; Parkinson's disease; asthma;
KW reproductive disorder; infertility; autoimmune disorder; gout; allergy;
KW inflammatory disorder; acquired immunodeficiency syndrome; uveitis;
KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;
KW diabetes mellitus; glomerulonephritis; irritable bowel syndrome;
KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
KW rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX WO200272830-A2.
XX
XX 19-SEP-2002.
XX
XX 08-FEB-2002; 2002WO-US003715.
XX
XX 09-FEB-2001; 2001US-0268111P.
XX
XX 23-FEB-2001; 2001US-0271175P.
XX
XX 08-MAR-2001; 2001US-0274503P.
XX
XX 09-MAR-2001; 2001US-0274552P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR;
XX Ding L, Xu Y, Gierzen KJ, Tang TY, Lal PG, Duggan BM, Burford N;
XX Lu DAM, Richardson TW, Tran UK, Khare R, Walia NK;
XX WPI; 2002-723356/78.
XX
XX N-PSDB; ABS78645.
XX
XX New human proteins associated with cell growth, differentiation and
XX death, useful for diagnosing, treating or preventing autoimmune or
XX inflammatory disorders (e.g. AIDS, allergy or anaemia), cancer,
XX atherosclerosis or hepatitis.
XX
XX Claim 1; Page 144-145; 181pp; English.
XX
XX The invention relates to an isolated polypeptide comprising CGDD1-12
XX (cell growth, differentiation and death), a naturally occurring amino
XX acid sequence at least 90% identical to CGDD, a biologically active
XX fragment or an immunogenic fragment. Also included are the
XX polynucleotides encoding CGDD1-12, a recombinant polynucleotide
XX comprising a promoter sequence operably linked to the CGDD
XX polynucleotides, a cell transformed with the recombinant polynucleotide,
XX a transgenic organism comprising the recombinant polynucleotide, an anti-
XX CGDD antibody, screening for compounds which bind to/modulate or are
XX ant/agonists of CGDD or alter the expression of CGDD polynucleotide and a
XX CGDD polynucleotide microarray. The polypeptides, polynucleotides,
XX agonists and antagonists are useful for diagnosing, treating or
XX preventing disorders associated with aberrant expression of CGDD,
XX particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis,
XX cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia
XX vera, psoriasis, primary thrombocytopaenia or cancer), developmental
XX disorders (e.g. renal tubular acidosis, anaemia or mental retardation),
XX neurological disorders (e.g. Alzheimer disease, Parkinson's disease or
XX epilepsy), reproductive disorders (e.g. infertility or a disruption in
XX the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,
XX (acquired immunodeficiency syndrome) allergies, asthma, autoimmune
XX thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,
XX glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis,
XX osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis,
XX uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic
XX infections. They are also useful in the assessment of the effects of
XX exogenous compounds on the expression of nucleic acid and amino acid
XX sequences of proteins associated with CGDD. The present sequence
XX represents a CGDD protein
XX
XX Sequence 468 AA;
XX
Query Match 22.4%; Score 560; DB 5; Length 468;
Best Local Similarity 32.5%; Pred. No. 1.4e-39;
Matches 154; Conservative 75; Mismatches 191; Indels 54; Gaps 16;


```
QY 1 MACSLKDELICSLISYQDPVSLGCEHYFCRCITTEHWVROEAQOARDCECRRTAEP 60
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6 LSTNLQBEATCAICLDYTDPTDVMTCGHNFRCICIRCWGQPE--GPYACPECELSFQR 63
QY 61 ALAPSLKLANIVERYSSFPDLDAILNARRAARP-----COAH-DKVKLFCLTDRLALCF 112
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
64 NLARNRPLAKWAE-----ARRLHPSPVPQGVCPAHPREPLAAFCGDELRLICA 112
QY 113 FDEPALHQBHOVGTGIDAFDELQRELKDQALQDSEREHTEALQLLKRLQLAET----X 168
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
113 ACERSGEHWAHRVRLPQDAAEADLKAKLEKSLHEH----RKQMQLLFOAQADETCLVWQ 168
QY 169 SSTKSLTTTGEAEFERHLRLRRQKAMLEADTARTLTDIEQVQVYSOQLRKVQEG 228
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
169 KWVESQONVGEFERLRLRAEEQQLQRLKEEELEVLPRREGAHLGQQ----- 221
QY 229 AQILQERLAETDRFTLAGVASLSERLKG---KIHETNLITYEDFTSKYTGLOV-TIWK 284
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
222 SAHLAEILAELEGRCLPALGLQD-IKDALLRRVDQVKLOPPE-----VVPMEIRTVCR 274
QY 285 --SLFQDIHPVPAALTDPGTAHORLILSDCTIVAYGNLHPQLQDSPKRFDFVEVSVIG 342
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
275 VPGLVETLRRFRGVTLPDPTANPELILSEDRSVQRGDLR-QALPDSPERFDGPCVIG 333
QY 343 SEAFSSGVHYWEVVVAETQWVIGLAHEAASRKGSIQIOPSRGFYCIWMHNGNOYSACTE 402
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
334 QERTSGRHWEEVVGORTSWALGVCRNVNRKEGELSGAGNWILLVFL-GSYNNSER 392
QY 403 PWRNLNVRDKLVGFIDYDQGLLIFYNADMSWLYTFRE-KPPGKLCYSFSP 455
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
393 ALAPL--RDPPRRVGIIFYEAGHLSFYSATDGSLLFIFFPIPSGTLRLPLFSP 444

RESULT 14
ID AAR15148
XX AAR15148 standard; protein; 475 AA.
AC AAR15148;
XX
XX 14-FEB-1992 (first entry)
XX Ro/SSA autoantigen.
XX Autoantibody; autoantigen; SLE; systemic lupus erythematosus.
XX Homo sapiens.
XX WO9117171-A.
XX 14-NOV-1991.
XX 07-MAY-1990; 90US-00520270.
XX 07-MAY-1990; 90US-00520270.
XX (OKLA-) OKLAHOMA MED RES FO.
XX Frank MB, Itoh K;
XX WPI; 1991-353712/48.
XX N-PSDB; AAQ14798.
XX
XX DNA encoding protein in human Ro-SSA ribo-nucleoprotein complex - useful
XX for diagnosing auto-immune disorders or presence of auto-antibodies.
XX Disclosure; Fig 2; 4lpp; English.
XX A cDNA library (from human thymus mRNA) in lambda gtl1 was screened with
XX serum from a patient having systemic lupus erythematosus. Two clones were
XX reactive with sera (from a panel of lupus patients) which contd.
XX autoantibodies against 52 kD protein. Both the cDNA and the protein
XX expressed from it, or portions of it, are useful as diagnostic agents in
```

```
CC the identification of patients having autoantibodies and in the
CC identification and analysis of the structural and functional properties
CC of the autoantigen and for application in immunotherapeutic regimens
XX
XX Sequence 475 AA;
Query Match 22.1%; Score 552.5; DB 2; Length 475;
Best Local Similarity 31.3%; Pred. No. 6.6e-39;
Matches 150; Conservative 88; Mismatches 208; Indels 33; Gaps 14;
QY 7 DELICSLISYQDPVSLGCEHYFCRCITTEHWVROEAQOARDCECRRTFAEPALAPSL 66
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
12 EEVTCPLDPPFVPEVSIIECHSFCQECISQ----VGKGGSVCPVCRQRLKLNLRN 67
QY 67 KLANIVERYSSFPDLDAILNARRAARPQOAH-DKVKLFCLTDRLALCFDEPALHQBHOV 125
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
68 QLANMNNLKEISQEA--REGTQGERCAVHERLHLFCEKDQKALCVWCAQSRKHROHAM 125
QY 126 TGIDDAFDELQRELKDQALQDSEREHTEALQD--LKRQLAETKSTKSLRTTIGEAF 182
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
126 VPLEAAQETQEKLVQALGELR-RKQELAEKLEVEIAIKR--ADWKKTIVETQKSRHAEF 182
QY 183 ERLHRLRRQKAMLEADTARTLTDIEQVQVYSOQLRKVQEGAQILQERLAETDRH 242
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
183 VQKNFVLEBEQRLQELKDEREQRLILGEKAKLAQO-----SQALQELISELDDR 235
QY 243 TFLAGVASLSERL--KGIHETNLITYEDFTSKYTGLOVITWKSIFQD--IHPVPAALT 298
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
236 CHSSALELQEVITVLERSESNLKDLDITSPELRSVCHVPLGKMLRTCAVH----IT 290
QY 299 LDPCTAHORLILSDCTIVAYGNLHPQLQDSPKRFDFVEVSVIGSEAFSSGVHYWEVVVA 358
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
291 LDPDTANPWLILSEDRRQVRLGDTQ-QSIPGNERFDSYPMVLGAQHFGHSGKHYWEVDVT 349
QY 359 EKTQWVIGLAHEAASRKGSIQIOPSRGFYCIWMHNGNOYSACTEPWTRLNVRDKLVGV 418
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
350 GKEAWDLGVCRDSVRRKGHFLSSKSGFTIWLWNKQKYEAGTYPTPLHLQVPPCQVGI 409
QY 419 FLDYDQGLLIFYN-ADMSWLYTFRE-KPPGKLCYSFSPGQSHANGKNVOPRLINTVRI 475
Dd : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
410 FLDYEAGWVSFYNTIDHGSILYFSFCAFTGLRPFPSFG-FNDGGKNTAPLTLCPLNI 467

RESULT 15
ID AAM48396
XX AAM48396 standard; protein; 485 AA.
AC AAM48396;
XX
XX 13-MAY-2002 (first entry)
XX Human SSA-56kDa protein.
XX Human; SSA-56kDa; virucide; anti-HIV; immunosuppressive; dermatological;
XX antiinflammatory; hepatotropic; Ro/SSA-like protein; autoimmune disease;
XX systemic lupus erythematosus; SLE; Sjogren syndrome; RNA virus infection;
XX HIV infection; hepatitis B; hepatitis C; chronic pathogen infection;
XX transgenic animal.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 16..54
XX /note= "zinc finger domain"
XX Region 91..123
XX /label= B Box
XX /note= "Cysteine and histidine rich region"
XX Domain 190..245
XX /note= "Leucine zipper"
XX
XX WO200188128-A1.
XX 22-NOV-2001.
```

Job time : 57 secs

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XX 12-MAR-2001; 2001WO-FR000725.
XX
XX 17-MAY-2000; 2000FR-00006315.
XX
XX (ISTA-) ISTAC.
XX (INSP ) INST PASTEUR LILLE.
XX
XX Bahr G, Cocude C, Capron A;
XX
XX WPI; 2002-066692/09.
XX N-PSDB; ABA98677.
XX
XX New human Ro/SSA-like polypeptide, useful for treatment, prevention and
XX diagnosis of e.g. autoimmune disease and viral infection, also related
XX nucleic acid and antibodies.
XX
XX Claim 1; Page 86-88; 109pp; French.
XX
XX The present sequence is a novel human Ro/SSA-like protein, SSA-56 kDa.
XX The coding sequence for SSA-56 protein can be used for the diagnosis or
XX monitoring of autoimmune diseases (particularly systemic lupus
XX erythematosus, SLE, or Sjogren syndrome), infections by RNA viruses
XX (particularly HIV or hepatitis B and C) or chronic pathogen infections
XX associated with autoimmune manifestations. The coding sequence for SSA-56
XX protein can also be used to generate transgenic animals for studying the
XX aetiology of Ro/SSA-like protein-related diseases or effects of viral
XX infection on expression of Ro/SSA-like protein
XX
XX Sequence 485 AA;
XX
Query Match 22.0%; Score 550.5; DB 5; Length 485;
Best Local Similarity 29.3%; Pred. No. 1e-38;
Matches 150; Conservative 94; Mismatches 181; Indels 87; Gaps 17;
QY 4 SLKDELLCSICLSIYQDPSLGCHEYFCRCRCITEHW-VRQEAQG-ARDQCECRRTFAEPA 61
Db 9 AIVEVACPICTMFRPMSIDCGSFCHSGLWEIPGESQNWGYTCPLCEAPVQPRN 68
QY 62 LAPSLKLANIVERYSSFPDLAINARRAAPCOAH-DKVKLFCLTDRALLCFFCDEPAIH 120
Db 69 LRPNQLANVVEKVLRLHPGMGLK--GDLCEHGEKLMKFKEDVLMCEACSQSPRH 126
QY 121 EHQVTGIDDAFDELQRELKQALQDSERHTEALQLKQLAET-KSSTKSRLRTTIG 179
Db 127 EAHSVPMEDVAVWEYKWEHLEHLK-KQSEAWKLEVGERRKRTATWIKIVETRKQSIY 185
QY 180 EAFERHLRLRRQKAMLEELADTARTLTDTQKVQYSQQLR---KVQEGAQILQER 235
Db 186 WEFEKYQRLLEKKQPPH-RQLGAEVAALASQREAAETMQKLELNHSELIOQSQVLWRM 244
QY 236 LAETDRHTFLAGVSLSERLKGKIHETNLTIEDFTPTSKYTGPLQYTIWKSLEFQDI----- 290
Db 245 IAE-----LKERSQRFVR-----W--MLQDIQEVLN 268
QY 291 -----HPVPAAL-----TLDPGTAHORLILSDCTIVAYG 320
Db 269 RSKSWLSQOPEPISLELTKDTCVLGRILKTYAADVRLDPTAYSRLLIVSDRKRVHYG 328
QY 321 NLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWVAVAEKQWVIQGLAHEAASRKGSIQI 380
Db 329 DTN-QKLDPNPERFYRNIVLSQCISGRHYWEVVGDRSEWGLGVCKQNVDRKEVVYL 387
QY 381 QPSRFYCIYIMHDGQYSACTEPWRLNVDRKLDKGVFLDYDQGLLIIFYNADDM-SWLY 439
Db 388 SPHYGFWRILRKNGNEYRAGTDEYFILSLPVPFRVGFVDYEAHDIISFYNVTDYGSHTF 447
QY 440 TF-REKFGPKLCYSRPSGOSHANGKVVQLRI 470
Db 448 TFRYFPFGRLLPYFSPCYIS-ICTNNTAPLAI 478
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:05:45 ; Search time 19 seconds
(without alignments)
1290.649 Million cell updates/sec

Title: US-09-927-091-1
Perfect score: 2504
Sequence: 1 MACSLKDELLCSICLSIYOD.....GQSHANGKNVQLINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546.5	21.8	487	2	US-08-724-394A-7
2	486	19.4	485	2	US-08-724-394A-8
3	427.5	17.1	781	4	US-09-486-147-3
4	421	16.8	179	4	US-09-486-147-38
5	396	15.8	178	4	US-09-486-147-37
6	364.5	14.6	413	4	US-09-663-600A-198
7	348	13.9	183	4	US-09-486-147-36
8	339	13.5	584	4	US-09-910-174B-16
9	339	13.5	584	4	US-09-620-461-16
10	335.5	13.4	184	4	US-09-486-147-35
11	329	13.1	513	4	US-09-910-174B-18
12	329	13.1	513	4	US-09-620-461-18
13	321	12.8	610	2	US-08-724-394A-5
14	316.5	12.6	527	4	US-09-910-174B-10
15	316.5	12.6	527	4	US-09-620-461-10
16	315.5	12.6	529	4	US-09-910-174B-13
17	315.5	12.6	529	4	US-09-620-461-13
18	312.5	12.5	181	4	US-09-486-147-5
19	311.5	12.4	174	4	US-09-486-147-41
20	307.5	12.3	523	4	US-09-910-174B-11
21	307.5	12.3	523	4	US-09-620-461-11
22	305.5	12.2	540	2	US-08-724-394A-4
23	303	12.1	185	4	US-09-486-147-39
24	299	11.9	581	2	US-08-724-394A-2
25	295.5	11.8	581	2	US-08-724-394A-3
26	293	11.7	526	4	US-09-910-174B-9
27	293	11.7	526	4	US-09-620-461-9

Sequence 15, Appl
Sequence 15, Appl
Sequence 1, Appl
Sequence 6, Appl
Sequence 171, Appl
Sequence 5, Appl
Sequence 43, Appl
Sequence 104, Appl
Sequence 5, Appl
Sequence 40, Appl
Sequence 42, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 44, Appl
Sequence 4209, Ap
Sequence 468, App
Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-724-394A-7
; Sequence 7, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF INVENTION: Sequences and Antibodies Thereto
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..487
; OTHER INFORMATION: /note= "52 kD Ro"
US-08-724-394A-7

ATTORNEY/AGENT INFORMATION:
NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..485
OTHER INFORMATION: /note= "RoRet"
US-08-724-394A-8

Query Match 19.4%; Score 486; DB 2; Length 485;
Best Local Similarity 29.3%; Pred. No. 2.5e-37;
Matches 137; Conservative 80; Mismatches 213; Indels 38; Gaps 12;

QY 5 LKDELCSICLSIYQDPVSLGCHYFCRCITTEHWVROEAQAGARD---CPECRRTEAF 60
DB 10 MMEATCSICLSIMTNFVINGCHSYCHLCITDFFKNPSQKQLRQETFCPCQCRAPFHM 69
QY 61 ALAPSLKLANIYERYSFPDLALNARRAARPCOAH-DKVKLFLCLTDRLALLCFPCDEPAL 119
DB 70 SLRPNKQLSLBALKE--TDQEMXXXXXXSCHEGEQHFLECEDEGQLICWRCERAPQ 127
QY 120 HEHQVGTGDDAFDELQRELKQLOALQDSEREHTALQLLKRQLAETKSTKSLRTTIG 179
DB 128 HKGHTALVEDVCOQYKEKQAVTKLQLEDRECTEQLSTAMRITKWEKVQIQOKIR 187
QY 180 EAFERHLRLRERQKAMLELEADTARTLT---DIEQVORYSQQLR-----KVQEG 228
DB 188 SDFKNLQCLFHEBEKSYLWLEKEBOQTLRLRDYEAGLGLKSNELKSHILEEKKQGS 247
QY 229 AQILQERLAETDRHTFLAGVASISERLKGKHETNLTYEDFPTSKYTGPIQYTIWKSIFQ 288
DB 248 AQKLLQVNDT-----LSRWAVKLETSEAVSLELHTMCNVSKLYFDVKMLRS 296
QY 289 DIHPVPAALTDPCTAHQRLILSDDCCTIVAYGNLHPQLOD-SPKRFDEVSVLGSEAFS 347
DB 297 --HQV--SVTLDPDPAHHEILSEDRRQVTRG--YTQENQDTSRRRTAFPCVLGCEGT 350
QY 348 SGVHYEVVVAEKTOQWVIGLAHEAASRKSIGIQPSGFYCIYVMDGNQYSACTEPWTRL 407
DB 351 SGRRYFEVDVGEGTGMDLGVCMENVORGTGKQBPQSGFWTLRCKKKGYVALTSPTSL 410
QY 408 NVRDKLVGVFLDYDOGLLIFYNADDMWS-WLYTF-REKFGKLCYSF 453
DB 411 HLHEQPLVLGFLDYEAGVSVFYNGXTGCHIFTFPKASFDTLRPYF 458

RESULT 3
US-09-486-147-3
; Sequence 3, Application US/09486147
; Patent No. 6627745
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary, Department of Health and Human
; APPLICANT: Services
; APPLICANT: Daniel L. Kastner
; APPLICANT: Ivona Aksentijevich
; APPLICANT: Michael Centola
; APPLICANT: Zuoming Deng
; APPLICANT: Raman Sood
; APPLICANT: Francis S. Collins
; APPLICANT: Trevor Blake
; APPLICANT: P. Paul Liu

Query Match 21.8%; Score 546.5; DB 2; Length 487;
Best Local Similarity 30.4%; Pred. No. 4.7e-43;
Matches 150; Conservative 92; Mismatches 202; Indels 49; Gaps 16;

QY 7 DELICSICLSIYQDPVSLGCHYFCRCITTEHWVROEAQAGARD---CPECRRTEAF 57
DB 12 BEVTCPICLDPFVEPVSTEGCHSFCQECIS-----QVGKGGGXXXXXXVCPVCRORF 66
QY 58 AEPALAPSLKLANIYERYSFPDLALNARRAARPCOAH-DKVKLFLCLTDRLALLCFPCDE 116
DB 67 LKLNLRPNRQLANVNNLKEISQEA-REGTOGERCAVHGERLHLFCEDKQKALCWVCAQ 124
QY 117 PALHEHQHVTGDDAFDELQRELKQLOALQDSEREHTALQJ---LKQLAETKSTKS 173
DB 125 SKRHRDAMVPLEEAAQYQEKLOVALGELR-RKQELAEKLEVEIAIKR--ADWKKTVET 181
QY 174 LTTTIGEAFERHLRLRERQKAMLELEADTARTLTDBOKVORYSQQLRKVQEGAQIILQ 233
DB 182 QKSRHAEPVQKNFLVEEQQQLQLEKDEREQRLIGKEKAKLAQ-----SQALQ 234
QY 234 ERLAETDRHTFLAGVASISERL-----KGKHETNLTYEDFPTSKYTGPIQYTIWKS 286
DB 235 ELISELDRCHSALELLEQVIVLERSSESNLKDLDITSPELRSVCHV-PXXXXGLKKM 293
QY 287 FQD--IHPVPAALTDPCTAHQRLILSDDCCTIVAYGNLHPQLODSPKRFDEVSVLGSE 344
DB 294 LRTCAVH-----ITLDPDTANPWLILSEDRRQVRLGDTQ-QSIPGNEERFDSYPMVLGAQ 347
QY 345 AFSSGVHYEVVVAEKTOQWVIGLAHEAASRKSIGIQPSRGFYCIYVMDGNQYSACTEPW 404
DB 348 HFHSGRHYEVDVTGKEAWDLGVCRDSVRKKGHLLSSKSGFWTIWLNKQKYEAGTYQ 407
QY 405 TRLNVRDKLVGVFLDYDOGLLIFYN-ADDMWSLYTFRE-KPFGKLCYSFSPGQSHANG 452
DB 408 TPLHLQVPCQGVIFLDYAGWVSFYNTDHSGLIYSFSFCACTGTLRPFPSFG-FNDGG 456
QY 463 KNQQLRINTVRI 475
DB 467 KNTAPLTLCPLNI 479

RESULT 2
US-08-724-394A-8
; Sequence 8, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchibashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536

```
; APPLICANT: Deborah Gumucio
; APPLICANT: Robert I. Richards
; APPLICANT: Darrell O. Riche
; APPLICANT: No. 6627745man A. Doggett
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; FILE REFERENCE: 14014.0314U1
; CURRENT APPLICATION NUMBER: US/09/486,147
; PRIOR APPLICATION NUMBER: PCT/US98/17255
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: 60/056,217
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 781
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
US-09-486-147-3

Query Match      17.1%; Score 427.5; DB 4; Length 781;
Best Local Similarity 25.2%; Pred. No. 1.8e-31;
Matches 132; Conservative 79; Mismatches 168; Indels 145; Gaps 17;

QY 20 DPVSLGCHYRCR--RCITEHWVROEAQARD--CPECRTFF---AEPALAPSLKANIV 72
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
321 PDVGTCTVRDCSPFEAVSGH---PQASGSRSPGCRQDSHERKSPGSLSPQ----- 370
QY 73 ERYSSFPLDAILNARRAARPCQAHDK--VKLFCLTDRALLCFDCDEPALHSHQVTVGDD 130
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
371 -----PLP-----QCKRHLKQVQLFCEDHDEPICLISLSEHGHVRPREE 414
QY 131 AFDELORELKDQALQDSEHREHTALQLKQLAETKS-----STKSLRTTIGEAFFRL 185
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
415 VALBHKKKIQKLEHLKKLRKSGEE---QRSYGEKAVSFLKQTEALKQVQRKLBQV 469
QY 186 HRLLRERQ-----KAMLEELLEADTAR----- 206
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
470 YFLEQOEHFVVASLEDVGQMVQIRKAYDTRVSDIALLDALLGELEAKECQSEWELLQ 529
QY 207 -----TLTDIEQKVQYSQQLRKVQECQAQLQERLAETDRHTFLAG 247
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
530 DIGDILHRAKIVPPEKWTTPQEIQKQIQLLHQKSEFVEKSKYFSETL-RSEMEFP--- 585
QY 248 VASLSERLKGKIHETNLTIEDFTPTSKYTGPLQYTIWKSLFQDIHPVPAALFLDPGTAHQ 307
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
586 --NVPELIGAQAHAVN-----VILDAETAYPN 610
QY 308 LILSDDDCTIVAYGNLHPQLDPSKPRFDEVSVLGSEAFSSGVHYWVVAEKTQWVIGL 367
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
611 LIFSDDLKSLVGLGNK--ERLPDGPQRDFSCIIIVLGSPSFLSGRRYWEVEVDGDKTAWILGA 669
QY 368 AFEAASRKSIIQPSRGFYCIVMHDGNQYSACTEPWTRNLNVRDKDKVGVFLDYDQGLL 427
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
670 CKTSISRKGNMTLSPENGYWVIMNKENEYQASSVPFTRLLIKEPPRRVGIFFVDIRVGS 729
QY 428 IFYNADMSWLYTPRE-KFPGKLCSPSPGQSHANGKNVQPLRI 470
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
730 SFYNTVARTASHIYTFASCSFSGLQPIFSPG-TRDGGKNTAPLTI 772

RESULT 4
US-09-486-147-38
; Sequence 38, Application US/09486147
; Patent No. 6627745
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary, Department of Health and Human
; APPLICANT: Services
; APPLICANT: Daniel L. Kastner
; APPLICANT: Ivona Aksentijevich
; APPLICANT: Michael Centola
; APPLICANT: Zuoming Deng
; APPLICANT: Raman Sood
; APPLICANT: Francis S. Collins
; APPLICANT: Trevor Blake
; APPLICANT: P. Paul Liu
; APPLICANT: Deborah Gumucio
; APPLICANT: Robert I. Richards
; APPLICANT: Darrell O. Riche
; APPLICANT: No. 6627745man A. Doggett
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; FILE REFERENCE: 14014.0314U1
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/US98/17255
```

```
; APPLICANT: Ivona Aksentijevich
; APPLICANT: Michael Centola
; APPLICANT: Zuoming Deng
; APPLICANT: Raman Sood
; APPLICANT: Francis S. Collins
; APPLICANT: Trevor Blake
; APPLICANT: P. Paul Liu
; APPLICANT: Deborah Gumucio
; APPLICANT: Robert I. Richards
; APPLICANT: Darrell O. Riche
; APPLICANT: No. 6627745man A. Doggett
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; FILE REFERENCE: 14014.0314U1
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/US98/17255
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: 60/056,217
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Pleurodeles Waltl
US-09-486-147-38

Query Match      16.8%; Score 421; DB 4; Length 179;
Best Local Similarity 47.7%; Pred. No. 7.3e-32;
Matches 84; Conservative 28; Mismatches 62; Indels 2; Gaps 2;

QY 295 AALTDPGTAHQRLILSDCTIVAYGNLHPQLDPSKPRFDEVSVLGSEAFSSGVHYWE 354
Db 1 APLTLDPNHTAHPNLVLSGLTSVKYTDI-KQQLDPNPKRFSCIIIVLGAEFGDSGKHWE 59
QY 355 VVAEKTQWVIGLHAHAASRKSIIQPSRGFYCIVMHDGNQYSACTEPWTRNLNVRDKLD 414
Db 60 VEVGNKTAWDVGMASESNNRKGKIKLNPKNGYAIWLRNGNAFKALSPSKTLNLTSPS 119
QY 415 KVGFLDYDQGLLIFYNADMSWLYTPREKFGKLCSPGQSHANGKNVQPLRI 470
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 KIGVLYDEGGQVSFYNADMSPIYTFNGSTFKLYPILSPFLQD-SGKNAEPLKL 174

RESULT 5
US-09-486-147-37
; Sequence 37, Application US/09486147
; Patent No. 6627745
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary, Department of Health and Human
; APPLICANT: Services
; APPLICANT: Daniel L. Kastner
; APPLICANT: Ivona Aksentijevich
; APPLICANT: Michael Centola
; APPLICANT: Zuoming Deng
; APPLICANT: Raman Sood
; APPLICANT: Francis S. Collins
; APPLICANT: Trevor Blake
; APPLICANT: P. Paul Liu
; APPLICANT: Deborah Gumucio
; APPLICANT: Robert I. Richards
; APPLICANT: Darrell O. Riche
; APPLICANT: No. 6627745man A. Doggett
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; FILE REFERENCE: 14014.0314U1
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/US98/17255
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QY 60 PALAPSLKLANIVERYSFFPILDAILNARRAARPCOAH-DKVKLFCLTDRALLCFCDDEPA 118
Db 66 EHLQANQHIANIYERLKEVKLSPDNGKKRDL--CDHGEKLLFFCKEDRKVICWLCERSQ 123
QY 119 LHEQHVTGIDDAFDELQRELKQALQDSREHTEALQLLKRLAETKSTK-----SL 174
Db 124 EHRGHHTVLTREVFKECEKQLQAVLRLKKEBEE---AEKLEADIREKTSWKYQVQPE 179
QY 175 RTTIGEAERLHRLRERQKMLELEADTATLTLDIEQKVQVQSLRKVQV-----227
Db 180 RQRIQTFDQSRILNNEEQRELQRLBEEKTLQKFAEDELVOQKQVRELSDVBC 239
QY 228 -----GAQILQERLAETDRHTFLAGVASLSE--RLKGIHETNLTYEDFPTSKYTGPLYQ 280
Db 240 RQWSTMELLQD-----MSGIMKWSIWLK-----KPKMWSKKLKTVFHAPDLR 285
QY 281 TIWKSIFQDIHVPV---AALTLDPGTAHORLLISDDCTTIVAYGNLHPQLQDSPKRFDVE 337
Db 286 ML--QMFRELTAVRCYVVDVTLNSVNLNLVLSEDRQVIVSVPWPFQYN-----335
QY 338 VSVLGSEAFSSGVHYWEVVAEKTQWIG-----LAHEAASRKG-SIQIOPSR 384
Db 336 YGVLSGQYFSSGRKHWEVDVSKTAMILGVCTYSRHKYVVRRCANRONLYTKYRPLF 395
QY 385 GFYCIVMHDGNOYSA 399
Db 396 GYVIGLQNKCKYGA 410

RESULT 7
US-09-486-147-36
; Sequence 36, Application US/09486147
; Patent No. 6627745
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary, Department of Health and Human
; APPLICANT: Services
; APPLICANT: Daniel L. Kastner
; APPLICANT: Ivona Aksentijevich
; APPLICANT: Michael Centola
; APPLICANT: Zuoming Deng
; APPLICANT: Raman Sood
; APPLICANT: Francis S. Collins
; APPLICANT: Trevor Blake
; APPLICANT: P. Paul Liu
; APPLICANT: Deborah Gumucio
; APPLICANT: Robert J. Richards
; APPLICANT: Darrell O. Rieke
; APPLICANT: NO. 6627745man A. Doggett
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; TITLE OF INVENTION: FAMILIAL MEDITERRANEAN FEVER
; FILE REFERENCE: 14014.0314UI
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/US98/17255
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: 60/056,217
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./ No. 6627745e =
; OTHER INFORMATION: Synthetic construct
US-09-486-147-36
Query Match 13.9%; Score 348; DB 4; Length 183;
Best Local Similarity 42.9%; Pred. No. 6.2e-25;
Matches 75; Conservative 28; Mismatches 68; Indels 4; Gaps 3;

QY 297 LTLDPGTAHORLLISDDCTTIVAYGNLHPQLQDSPKRFDVEVSVLGSEAFSSGVHYWEV 356
Db 3 MLLDPTSAHPNHLSDGLTSVRYGE-NKLSLDPNPKAFSCCIIVLGSGQFDSGRHYWEYE 61
QY 357 VAEKTQWVIGLAHEAASRKGSIQIOPSRGFYCIVMHDGNOYSACTEPTRLNVRDKLV 416
Db 62 VGDKTAWDVCMASSESSNRKGIKLNPKNGYWAIVLWNGNAYKALESPSKSLSSHPKRI 121
QY 417 GYFLDYDQGLLIYFNAADDMSWLYTREKPKGLCSYFSPQSHANGKNVQPLR 469
Db 122 GYVDYEGQIGSFYNADDMTIIYTFNATTEKLYPYLSP-FLHDSGNVDPLR 173

RESULT 6
US-09-663-600A-198
; Sequence 198, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouguerelet, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 198
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37...-1
US-09-663-600A-198
Query Match 14.6%; Score 364.5; DB 4; Length 413;
Best Local Similarity 26.4%; Pred. No. 6.2e-26;
Matches 115; Conservative 79; Mismatches 170; Indels 71; Gaps 15;
QY 4 SLKDELICSLCYQDPVSLGCHYFCRCRITETHWROEA---QCARDCPCRRTFAE 59
Db 8 NVQSEVTCPICLLEITLPLSDCGHSLCRACITVS--NKEAVTSMGKSGSCPCVGISYF 65

Db 5 LDAETAYENLIPSDLDKLVRLGNKW-ERLPDGPQFQDSCIIIVLGSPFSLSGRRYVEVVG 63
QY 359 EKTQWVIGLAHAASRKGSIQIOPSRGFYCIYMHGNOYSACTEPWTRLNVRDKLDKGVG 418
Db 64 DXTAMILGACKTSISRKGNMTPSPENGYVVMIMKENEYQASSVPPTLLIKEPPKRVGI 123
QY 419 FLDYDQGLLIFYNADDMSLYTFRE-KFPGKLCVSFSPQOSHANGKNVOPLR1 470
Db 124 FVDYRVGSISFYVWTVARSHIYTFASCSFSGPLQIPFSPG-TRDGGKNTAPLTI 175

RESULT 11

US-09-910-174B-18
Query Match 13.1%; Score 329; DB 4; Length 513;
Best Local Similarity 34.1%; Pred. No. 2e-22;
Matches 89; Conservative 40; Mismatches 86; Indels 46; Gaps 7;
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-18
; APPLICANT: Manning, Stephen
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT FILING DATE: 2001-07-20
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-18

QY 202 ADTARTLTDI-----EQKVORYSQQLRKVQEGQAIIQERLAETDRHTFLAGVA 249
Db 250 AALARTLPVLLLLGGAGYFLWQQEKKYQPRKKRE--QELREMAWSTMKQEQSTRVK 307
QY 250 SLSE-----RLKGKIHTNLTYEDFTSKYTGLOQYTIW-KSLFQDIHPVPAAALTD 300
Db 308 LLEELRWSRISQVASRGHERSA-----YNEWKKALFK-----PADVILD 345
QY 301 PGTAHQRLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWEVVAEK 360
Db 346 PKTANPILLVSEDQSRVQRAK-EPQDLPDNPFENHMYCVLGCESTISGRHYWEVVGDR 404
QY 361 TQWVIGLAHAASRKGSIQIOPSRGFYCIYMHGNOYSACTEPWTRLNVRDKLDKGVGFL 420
Db 405 KEWHIGVCSKNVQKGVKMTPENGFWMTGLTDGNKYRTLTPRTNLKLPKPKKVGVL 464
QY 421 DYDQGLLIFYNADDMSLYTF 441
Db 465 DYETGDISFYNAVDSGHITF 485

RESULT 12

US-09-620-461-18
Query Match 13.1%; Score 329; DB 4; Length 513;
Best Local Similarity 34.1%; Pred. No. 2e-22;
Matches 89; Conservative 40; Mismatches 86; Indels 46; Gaps 7;
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-18
; APPLICANT: Manning, Stephen
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-18
Query Match 13.1%; Score 329; DB 4; Length 513;
Best Local Similarity 34.1%; Pred. No. 2e-22;
Matches 89; Conservative 40; Mismatches 86; Indels 46; Gaps 7;
QY 202 ADTARTLTDI-----EQKVORYSQQLRKVQEGQAIIQERLAETDRHTFLAGVA 249
Db 250 AALARTLPVLLLLGGAGYFLWQQEKKYQPRKKRE--QELREMAWSTMKQEQSTRVK 307
QY 250 SLSE-----RLKGKIHTNLTYEDFTSKYTGLOQYTIW-KSLFQDIHPVPAAALTD 300
Db 308 LLEELRWSRISQVASRGHERSA-----YNEWKKALFK-----PADVILD 345
QY 301 PGTAHQRLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWEVVAEK 360
Db 346 PKTANPILLVSEDQSRVQRAK-EPQDLPDNPFENHMYCVLGCESTISGRHYWEVVGDR 404
QY 361 TQWVIGLAHAASRKGSIQIOPSRGFYCIYMHGNOYSACTEPWTRLNVRDKLDKGVGFL 420
Db 405 KEWHIGVCSKNVQKGVKMTPENGFWMTGLTDGNKYRTLTPRTNLKLPKPKKVGVL 464
QY 421 DYDQGLLIFYNADDMSLYTF 441
Db 465 DYETGDISFYNAVDSGHITF 485

RESULT 13

US-08-724-394A-5
Query Match 13.1%; Score 329; DB 4; Length 513;
Best Local Similarity 34.1%; Pred. No. 2e-22;
Matches 89; Conservative 40; Mismatches 86; Indels 46; Gaps 7;
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-724-394A-5
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Rudy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 01/957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

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/ LENGTH: 610 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..610
/ OTHER INFORMATION: /note= "BTF3"
US-08-724-394A-5

Query Match      12.6%; Score 321; DB 2; Length 610;
Best Local Similarity 34.7%; Pred. No. 1.5e-21;
Matches 82; Conservative 45; Mismatches 87; Indels 22; Gaps 8;

QY 218 YSQLRKVEGAQILQER-----LAETDRH-TFLAGVASLSERLKGKIHETNLTYEDPPTSKYTGPLQYT 270
Db 287 WRQKEKIALSRETEREREMKEMGYAATEQEISXXXXXXXXXREKLQEELKWKRIQY---- 342
QY 271 TSKYTGPLQYTIWK-SLFQDIHPVPAALTLDPGTAHQRLILSDCTIVAYGNLHPQP--- 326
Db 343 MARGEKSLAYEHWKALFK-----PADVILDPDTANAILLVSEDOQRSVQRAE-EPRDXXX 396
QY 327 LQSPKPRDVEVSLGSEAFSGVHYWVVAETQWVIGLAHEAASR-KGSIQIQPSRG 385
Db 397 LPDNPPEFEMRYCVLGCENFTSGRHYWEVEGDRKEMHIGVCSKNVERKKGWVKTPENG 456
QY 386 FYCIVMHDGNOYSACTEPTWRLNVRDKLDKVGVLFDYDQGLLIFYNADDMSWLYTF 441
Db 457 YWTGLTDGNKYRALTEPTNLKLPFPPRKVGIFLDYETGRISFYNATDGGSHIYTF 512

RESULT 14
US-09-910-174B-10
; Sequence 10, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-10

Query Match      12.6%; Score 316.5; DB 4; Length 527;
Best Local Similarity 33.3%; Pred. No. 3.2e-21;
Matches 89; Conservative 38; Mismatches 93; Indels 47; Gaps 11;

QY 222 LRKVEGAQILQERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDPPTSKYTGPLQYT 281
Db 269 INKLQEKKKILSGE-KEFERETREIALKELEKERVQKEEELQVKEK-----LQEE 317
QY 282 I-WKSLFQDIHPVPAALTLDPGTAHQRLILSD-----CTIVAYGNLHPQLODPSKRF 334
Db 318 LRWRTF--LHVD--VVLDPDTAHPDLFLSEDRSRVRCRPFRLGESVP----DNPERF 369
QY 335 DVEVSLGSEAFSGVHYWVVAETQWVIGLAHEAASRKGSIQIQPSRGFYCIVMHDG 394
Db 370 DSQPCVLGRESFASGKHYYEVEVENVETVGVCRDSVERKGEVLLIPQNGFWLEMHKG 429
QY 395 NQYSACTEPTWRLNVRDKLDKVGVLFDYDQGLLIFYNADDMSWLYT-----F 441
Db 430 -QYRAVSSPDRLPLKESLCRVGVFLDYVEAGDVSYNNRDRSHIYTCPSAFSPVRPFF 488
QY 442 R---EKFPGLCSYFSPQSHANGKV 465
Db 489 RLGCEDSPFIC-----PALTGANGVTV 511

Search completed: July 23, 2004, 15:09:01
Job time : 20 secs
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Db 430 -QYRAVSSPDRLPLKESLCRVGVFLDYVEAGDVSYNNRDRSHIYTCPSAFSPVRPFF 488
QY 442 R---EKFPGLCSYFSPQSHANGKV 465
Db 489 RLGCEDSPFIC-----PALTGANGVTV 511

RESULT 15
US-09-620-461-10
; Sequence 10, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-10

Query Match      12.6%; Score 316.5; DB 4; Length 527;
Best Local Similarity 33.3%; Pred. No. 3.2e-21;
Matches 89; Conservative 38; Mismatches 93; Indels 47; Gaps 11;

QY 222 LRKVEGAQILQERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDPPTSKYTGPLQYT 281
Db 269 INKLQEKKKILSGE-KEFERETREIALKELEKERVQKEEELQVKEK-----LQEE 317
QY 282 I-WKSLFQDIHPVPAALTLDPGTAHQRLILSD-----CTIVAYGNLHPQLODPSKRF 334
Db 318 LRWRTF--LHVD--VVLDPDTAHPDLFLSEDRSRVRCRPFRLGESVP----DNPERF 369
QY 335 DVEVSLGSEAFSGVHYWVVAETQWVIGLAHEAASRKGSIQIQPSRGFYCIVMHDG 394
Db 370 DSQPCVLGRESFASGKHYYEVEVENVETVGVCRDSVERKGEVLLIPQNGFWLEMHKG 429
QY 395 NQYSACTEPTWRLNVRDKLDKVGVLFDYDQGLLIFYNADDMSWLYT-----F 441
Db 430 -QYRAVSSPDRLPLKESLCRVGVFLDYVEAGDVSYNNRDRSHIYTCPSAFSPVRPFF 488
QY 442 R---EKFPGLCSYFSPQSHANGKV 465
Db 489 RLGCEDSPFIC-----PALTGANGVTV 511

Search completed: July 23, 2004, 15:09:01
Job time : 20 secs
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:04:50 ; Search time 17 Seconds
(without alignments)
2687.704 Million cell updates/sec

Title: US-09-927-091-1
Perfect score: 2504
Sequence: 1 MACSLKDELLCSICLSIYQD.....QQSHANGKNVQPLRINTVRI 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	31.1	624	2 S28418	probable zinc-bind
2	763.5	30.5	609	2 A43906	nuclear phosphopro
3	663.5	26.5	518	2 JC7387	testis-abundant fi
4	583	23.3	513	1 TVHURF	ret finger protein
5	572	22.8	506	2 S37583	RING finger protei
6	552.5	22.1	475	1 A37241	52K autoantigen Ro
7	472.5	18.9	477	2 JE0343	terf protein - rat
8	372.5	14.9	667	2 T09482	ring finger protei
9	370.5	14.8	438	2 T12494	hypothetical prote
10	364.5	14.6	667	2 T09013	RING finger protei
11	353.5	14.1	442	2 A57041	transcription regu
12	341	13.6	630	2 A49656	estrogen-responsiv
13	304.5	12.2	634	2 I49642	butyrophilin - bov
14	301.5	12.0	526	2 A37821	butyrophilin precu
15	293	11.7	526	2 S70587	regulatory protein
16	286.5	11.4	487	2 S65333	glioblastoma RING
17	276.5	11.0	365	2 A30891	hypothetical prote
18	259	10.3	551	2 JC7562	butyrophilin 1, B
19	258.5	10.3	801	4 TVHURE	butyrophilin 2, B
20	239.5	9.6	210	2 T46303	hypothetical prote
21	233	9.3	150	2 T28135	ring finger B-box
22	227	9.1	224	2 T28136	probable ataxia-te
23	224	8.9	732	2 T00082	hypothetical prote
24	213.5	8.5	638	2 JC7753	ring finger B-box
25	166.5	6.6	588	2 A49618	probable ataxia-te
26	161.5	6.4	331	2 T31998	hypothetical prote
27	161	6.4	698	2 T32840	hypothetical prote
28	158	6.3	375	2 T33778	hypothetical prote
29	158	6.3	375	2 F88947	protein C39F7.2 [i

30	155.5	6.2	574	2 S28275	hypothetical prote
31	155.5	6.2	974	2 E88549	protein F54G8.4 [i
32	145.5	5.8	412	2 D88072	protein ZK1240.1 [
33	145.5	5.8	808	2 T22363	hypothetical prote
34	142.5	5.7	675	2 T01112	photomorphogenesis
35	140.5	5.6	1812	2 I49350	breast/ovarian can
36	137.5	5.5	700	2 A61527	stonustoxin beta c
37	137	5.5	487	1 DBY18	DNA repair protein
38	133.5	5.3	560	2 A40044	PM1-1 protein - hu
39	133.5	5.3	589	2 A60198	My1 protein - huma
40	133.5	5.3	589	2 S42517	PML protein, splic
41	133.5	5.3	589	2 S44381	PML protein, splic
42	133.5	5.3	593	2 B40045	probable transcrip
43	133.5	5.3	633	2 S19244	gene My1 protein -
44	133.5	5.3	641	2 A40045	probable transcrip
45	133.5	5.3	802	2 S42518	PML protein, splic

ALIGNMENTS

RESULT 1

S28418
probable zinc-binding protein - Iberian ribbed newt
C:Species: pleurodeles waltl (Iberian ribbed newt)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000
C:Accession: S28418; S29476
R:Bellini, M.; Lacroix, J.C.; Gall, J.G.
EMBO J. 12, 107-114, 1993
A:Title: A putative zinc-binding protein on lampbrush chromosome loops.
A:Reference number: S28418; MUID:93154311; PMID:7679068
A:Accession: S28418
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-624 <BEL>
A:Cross-references: EMBL:L04190
R:Bellini, M.; Lacroix, J.C.; Gall, J.G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29476
A:Accession: S29476
A:Molecule type: mRNA
A:Residues: 1-263, 'LK', 266-624 <BE2>
A:Cross-references: EMBL:L04190; NID:g213867; PID:g213868
C:Comment: This DNA-binding phosphoprotein is enriched in nuclei of adult brain cells an
C:Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:158-207/Domain: RING finger homology <RNG>

Query Match	31.1%	Score	778	DB	2	Length	624
Best Local Similarity	35.6%	Pred. No.	5e-41				
Matches	171	Conservative	81	Mismatches	193	Indels	36
Gaps	9						
QY	7	DELLCSICLSIYQDPVSLGCEHYFCRCRTEHWVROAQAQARDCECRRTFAFPALAPSL	66				
Db	158	EDLTCLPLSRLEPVLLEGHNFCRCHIDKSM--ESASAFSCPECKEVLTKRYTNR	214				
QY	67	KLANIVERTSYSPFDLAINNARRAARPCQAHD-KVULFCLTDRALLCFDCEPALHEQHV	125				
Db	215	VLANLVKAAVGVKDKVFKP--EKCDERLERLFCCKDDGTACVICRDSKLHSHNF	271				
QY	126	TGIDDAFDELQRELKDLQAL-----ODSERHEALQLLKRLAETKSTKSL	174				
Db	272	LPQDVG----VYRQLIALVSPLETTKKNOKLKDQSKTSLHRENTVDCKHIEC	326				
QY	175	RTTIGFAFERLHRLRRQKAMLELEADTARTLTIDIEQKVORYSQOLRKVQGAQILOE	234				
Db	327	-----EFEKLHQFLREKAKWEDLNAREGLLKQMEANLVKMTDNCFEIEAISTQS	380				
QY	235	RLAETDRHTFLAGVASLSRL-----KGKIHETNLTYEDPPTSKYTPGLQYTIWKSIFQD	289				
Db	381	RLNESDFIAFLTDIKSFIEKCCBEHRKGVPAESVLNKLKSQGRFNPGLYLIWKLKSV	440				
QY	290	IHPVPAALTLDPCTAQRJLLSDCTIVAYGNLHPQLQDSPKRFDVEVSLGSEAFSSG	349				

Db 441 VQPGIAPLTLDPTAHNPLVLSGLTSVKYTDYTKQQLPDPNPKRPSQICILVIGAFDPSG 499
QY 350 VHYEVVVAETQWVIGLAHAASRKGSIQIOPGRGFCYIVMHDGNOYSACTETWTRLNV 409
Db 500 KHYMEVEVGNKTAMDVGWASSSSNRKGIKLNPKNGYWAIVLRNGNAFKALESFSLNL 559
QY 410 RDKLDKVGVDYFDQGLLIFYNADMSWLYTFREKPKGLCSYFSPGSHANGKNVQPIR 469
Db 560 TSXPSKIGVLDYEGQVSYFNADMSPLYTFNGSFTEKLYPYLSPFLQD-SGKNABPLK 618
QY 470 I 470
Db 619 L 619

RESULT 2
A43906
nuclear phosphoprotein xnf7 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C:Accession: A43906; S27947
R:Reddy, B.A.; Kloc, M.; Etkin, L.
Dev. Biol. 148, 107-116, 1991
A:Title: The cloning and characterization of a maternally expressed novel zinc finger nu
A:Reference number: A43906; MUID:92038424; PMID:1936552
A:Accession: A43906
A:Molecule type: mRNA
A:Residues: 1-609 <RED>
A:CROSS-references: EMBL:M63705; NID:g214914; PID:g214915
A:Note: sequence extracted from NCBI backbone (NCBIN:64515, NCBIP:64520)
C:Genetics:
A:Gene: xnf7
C:Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
P:141-190/Domain: RING finger homology <RNG>

Query Match 30.5%; Score 763.5; DB 2; Length 609;
Best Local Similarity 35.4%; Pred. No. 3.9e-40;
Matches 167; Conservative 88; Mismatches 200; Indels 17; Gaps 9;
QY 7 DELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAGQARDCEPCRRTFAPALAPSL 66
Db 141 BELTCLVELFDPVWVACGHNFPCSCIDKAW---EGQSFACPCRRSITDRKKTINR 197
QY 67 KLANIVERYSSFPDLAINARRARPCQAHDKVKLCFLTDRLALLCFDDEPALHQBQHV 125
Db 198 VLANLAKKAACFTPTPEKKTREPLEKSEHDERLKYCKDDGTLSCVICRDSLKASHNF 257
QY 126 TGIDDAFDELQRELKQALQDSERHTEALQLLKRLAETKSTKSL---RTTIGFAF 182
Db 258 LPILDVAVGVRELSAIVAPLEASLVY-TE--QLSSEQSDKIBQHNKNMSQYKEHITSEF 314
QY 183 ERHLRLRRQKAMLEADTARTLTDIEQVORYSQQLRQVQGAQILQERLAETDRH 242
Db 315 EKLHFLREERKLEQKEGNNLTPEMNNLVQWQESQDAIKKILSLAKERMEDTDSI 374
QY 243 TEL---AGVASLSERLKGKHETN-LTYEDFPTSKYTGLOQYTIWKSFLQDTHPVPAL 297
Db 375 SFLMDIKAFIDKQEQRAVISTGNLTLSKELCQGTGFKPIQYIMWKEKLSVIPSITPM 434
QY 298 TLDPGTAHQRLILSDDCITVAYGNLHPQIDSPKRDVEVSLGSEAFSGVHYWEVVV 357
Db 435 LLDPTSAPNHLHLSGLTSVRYGE-NKLSLDPNPKRFSQICILVIGSQQGDSGRHYWEV 493
QY 358 AETQWVIGLAHAASRKGSIQIOPGRGFCYIVMHDGNOYSACTETWTRLNVRDKLVG 417
Db 494 GDKTAMDVGWASSSSNRKGIKLNPKNGYWAIVLRNGNAFKALESFSLSHPRKIG 553
QY 418 VFLLDYDQGLLIFYNADMSWLYTFREKPKGLCSYFSPGSHANGKNVQPIR 469
Db 554 VYVDYEGQISFYFNADMSWLYTFNATFTKLYPYLSP-FLHDSGKNVDPIR 604

RESULT 3
JC7387
testis-abundant finger protein - human
C:Species: Homo sapiens (man)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7387
R:Orimo, A.; Yamagishi, T.; Tominaga, N.; Yamauchi, Y.; Hishinuma, T.; Okada, K.; Suzuki
Biochem. Biophys. Res. Commun. 276, 45-51, 2000
A:Title: Molecular cloning of testis-abundant finger protein/ring finger protein 23 (RNF
A:Reference number: JC7387
A:Contents: Testis
A:Accession: JC7387
A:Molecule type: mRNA
A:Residues: 1-518 <ORI>
A:CROSS-references: DBJ:AB046381
C:Comment: This protein, a member of the ring-B box-coiled coil-B30.2 protein family, p1
C:Genetics:
A:Gene: tfp
A:Map position: 6p21.3-6p22.1
A:Introns: 151/3; 183/3; 260/3; 268/2; 298/2; 337/1
C:Superfamily: rfp transforming protein; RING finger homology
C:Keywords: coiled coil; testis
Query Match 26.5%; Score 663.5; DB 2; Length 518;
Best Local Similarity 32.8%; Pred. No. 5.5e-34;
Matches 167; Conservative 85; Mismatches 196; Indels 61; Gaps 13;
QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAGQARD--CPECRRTFAPEA 61
Db 22 NLQVEASCSVCLEYLKEPVIIICGHNFCKACITRWEDLE---RDFPCVCRKTSRYRS 77
QY 62 LAPSILKLANIVERYSSFPDLAINARRARPCQAHDKVKLCFLTDRLALLCFDDEPALH 120
Db 78 LRPNQLGSMVE--IAKQLQAVKRIKIDESLCPQHEALSLFCYEQEAVCLICASHTH 135
QY 121 EQHQVTGIDDAFDELQRELKQALQDSERHTEALQLLKRLAETKSTKSLRTTIGE 180
Db 136 RHTVTVPLDDATCEYKEKLEKQLEPLEKQLEITRCKSSEKKPGELKRLVESRQOILR 195
QY 181 APERLHRLRRQKAMLEADTARTLTDIEQVORYSQQL-----RK 224
Db 196 EFEEHLRRLDEEQVLLSRLEEE---QDILQRLRENAHAHGDGDKRRDLAHLAEVEGKC 251
QY 225 VQEGAQILQERLAETDRH---TFLAGVASLSER---LKGKHETNLTVDFTPTSKYTG- 276
Db 252 LOSGFEMLKDVKSTLEKNIPRKGGSLSITCIPRDHALLGLVKEIN-RCEKVKTMETVS 310
QY 277 -----PLQY-----TIWKSFLQDTHPVPALTDPGTAHQRLILSDDCITVAYGN 321
Db 311 SIELEKNFSNFPQYFALRKILKLIADV-----TLDPTAHNPLVLSEDRKSVEFE 363
QY 322 LHPQIDSPKRDVEVSLGSEAFSGVHYWEVVAETQWVIGLAHAASRKGSIQIQ 381
Db 364 TLRLDLPDTPRRFTFPYCVLATEGFTSGRHYWEVGDGKTHWAVGCRDVSVRKGEUTPL 423
QY 382 PSRGGFCYIVMHDGNOYSACTETWTRLNVRDKLVGVDYDQGLLIFYNADMSWLYTF 441
Db 424 PETGVKRVLRWNGDKVAATTPFTPLHLKVPKRVGLFIDYEAGTLSFYNVNDRSHIYTF 483
QY 442 REKFPFGKLCYSFPGSHANGKNVQPIR 470
Db 484 TDIPTFKLWPLFYFG-IRAGKNAAPLTI 511

RESULT 4
TVHURF
ret finger protein - human
N:Alternate names: transforming protein rfp
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 19-Jan-2001
C:Accession: A28101
R:Takahashi, M.; Inaguma, Y.; Hiai, H.; Hirose, F.

Mol. Cell. Biol. 8, 1853-1856, 1988
A;Title: Developmentally regulated expression of a human "finger"-containing gene encode
A;Reference number: A28101; MUID:88246464; PMID:3380101
A;Accession: A28101
A;Molecule type: mRNA
A;Residues: 1-513 <TAK>
A;Cross-references: DDBJ:J03407; NID:g337371; PIDN:AAA36564.1; PID:g337372
C;Genetics:
A;Gene: GDB:RFP
A;Cross-references: GDB:511359; GDB:1391662

A;Map position: 6p22-6p21.3
C;Superfamily: rfp transforming protein; RING finger homology
C;Keywords: DNA binding; transforming protein; zinc finger
F;1-315/Product: transforming protein rfp (fragment) #status predicted <RET>
F;12-62/Domain: RING finger homology <RNG>
F;16-127/Domain: metal and nucleic acid binding #status predicted <TMN>
F;16-56/Region: zinc finger C3HC4 motif

Query Match 23.3%; Score 583; DB 1; Length 513;
Best Local Similarity 29.1%; Pred. No. 5.7e-29;
Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;

```
QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQAGARDPCPCRTFAEPALAP 64
Db 10 LQQTTCPCVCLQYFAEPMWLDGHNICCAACARCWGTAETNVS--CPQCRETFFQHRMP 67
QY 65 SLKLANIVERSSPFLDAILNARRARP-----COAH-DKVKLFLCTDRALLCFPC 114
Db 68 NRHLANTVQ-----LVQLTERPSGGMGVCEKREPLKLYCEEDQMPICVVC 118
QY 115 DEPALHEQHVGTGIDDAFDELQRELKQALQALQDSERHEALQLLKRQ-----LAE 166
Db 119 DRSREHRGHSVLPLEAVEGFEKQIQNL-----DHLKRVKDKKRRRAQGEQARAE 170
QY 167 TKSSTKSRTTIGAFERLHLRLB---RQKAMLELE-----ADTA 205
Db 171 LLSLTQWEREKIVWEFEQLYHSLKEHEYRLARLEELDIAIYNSINGAITQFSCNISHLS 230
QY 206 RLTLDIEQKVORYSQOLRKVQGAQILQERLAETDR-----HTFLAGV 248
Db 231 SLIAQLHEKQOQPTREL-----IQDLDGTLRSRAERIRPEWITPPDLOEKIHFAKQC 284
QY 249 ASLSERLKGKHETNLTYEDPFTSKYTPLOQYTIWKSIFQDIHPV---PAALTLDPGTAH 305
Db 285 LFLTESLK-----QFTEKQSDMEK--IQELREAQLYSVDVTLDPDTAY 326
QY 306 QRLTSDCTIVAYGNLHPQLODPSKRFVSVLGSFAFSSGVHYVWVVAEKTQWVI 365
Db 327 PSLTSLNLRQVRSYLIQ-QDLPDNPFRNLFPCLVGLSPCFIAGRHYWEVVGDKAKWTI 385
QY 366 GLAHEAASRRKSGSIQIQPSRGFYCIWHDGNQYSACTEPWTRLNVRDKLDKGVFLDYDQ 425
Db 386 GVCEDSVCRKGGVTSAPQNGFWAVSLWYKEYWALTSPMTALPLRTPLQRVGIFLDYDAG 445
QY 426 LLIFYNADMSWLYTF-REKFPKGLCSYFSPGQSHANGKNVQPLRI 470
Db 446 EVSFYNVTERCHTFTSHATFCGPVPYFS--LSYSGKSAAPLI 489
```

RESULT 5

S37583

RING finger protein rfp - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999

C;Accession: S37583

R;Takahashi, M.

Submitted to the EMBL Data Library, October 1993

A;Reference number: S37583

A;Accession: S37583

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-506 <TAK>

A;Cross-references: EMBL:X75343; NID:g406747; PIDN:CAA53092.1; PID:g406748

C;Superfamily: rfp transforming protein; RING finger homology
C;Keywords: zinc
F;5-55/Domain: RING finger homology <RNG>

Query Match 22.8%; Score 572; DB 2; Length 506;
Best Local Similarity 28.5%; Pred. No. 2.7e-28;
Matches 148; Conservative 88; Mismatches 190; Indels 94; Gaps 14;

```
QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQAGARDPCPCRTFAEPALAP 64
Db 3 LQQTTCPCVCLQYFVPMWLDGHNICCAACARCWGTAETNVS--CPQCRETFFQHRMP 60
QY 65 SLKLANIVERSSPFLDAILNARRARP-----COAH-DKVKLFLCTDRALLCFPC 114
Db 61 NRHLANTVQ-----LVQLTERPSGGMGVCEKREPLKLYCEEDQMPICVVC 111
QY 115 DEPALHEQHVGTGIDDAFDELQRELKQALQALQDSERHEALQLLKRQ-----LAE 166
Db 112 EPSREHRGHSVLPLEAVEGFEKQIQNL-----DHLRRVKDKKRRRAQGEQARAE 163
QY 167 TKSSTKSRTTIGAFERLHLRLB---RQKAMLELEADTARTITDIEQKVORYS----- 219
Db 164 LLSLTQWEREKIVWEFEQLYHSLKEHEYRLARLEELDIAIYNSINGAITQFSCNISHLS 223
QY 220 -----QQLRKVQGAQILQERLAETDR-----HTFLAGVASLSER 254
Db 224 GLIAQLHEKQOQPTRELQDIDGTLRSRAERIRPEWITPPDLOEKIHFAKCLIFLTS 283
QY 255 LKGKHETNLTYEDPFTSKYTPLOQYTIWKSIFQDIHPV---PAALTLDPGTAHQLILS 311
Db 284 LK-----QFTEKQSDMEK--IQELREAQLYSVDVTLDPDTAYPSLILS 325
QY 312 DDCITVAYGNLHPQLODPSKRFVSVLGSFAFSSGVHYVWVVAEKTQWVIGLAHEA 371
Db 326 DNLQVRSYLIQ-QDLPDNPFRNLFPCLVGLSPCFMAGRHYWEVVGDKAKWTIGVCDS 384
QY 372 ASRKGSIQIQPSRGFYCIWHDGNQYSACTEPWTRLNVRDKLDKGVFLDYDQGLLIFYN 431
Db 385 VCRKGGVTSAPQNGFWAVSLWYKEYWALTSPMTALPLRTPLQRVGIFLDYDAGEVSFN 444
QY 432 ADDMSWLYTF-REKFPKGLCSYFSPGQSHANGKNVQPLRI 470
Db 445 VTERCHTFTSHATFCGPVPYFS--LSYSGKSAAPLI 482
```

RESULT 6

A37241

52K autoantigen Ro/SS-A - human

N;Alternate names: Sjogren syndrome antigen A

C;Species: Homo sapiens (man)

C;Date: 07-Feb-1992 #sequence_revision 26-May-1995 #text_change 17-Mar-2000

C;Accession: A55642; A37241; A37240

R;Tsugu, H.; Horowitz, R.; Gibson, N.; Frank, M.B.

Genomics 24, 541-548, 1994

A;Title: The location of a disease-associated polymorphism and genomic structure of the
A;Reference number: A55642; MUID:95229155; PMID:7713506

A;Accession: A55642

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-475 <TSU>

A;Cross-references: GB:U13657

R;Itch, K.; Itch, Y.; Frank, M.B.

J. Clin. Invest. 87, 177-186, 1991

A;Title: Protein heterogeneity in the human Ro/SSA ribonucleoproteins. The 52- and 60-kD

A;Reference number: A37241; MUID:91086445; PMID:1985094

A;Accession: A37241

A;Molecule type: mRNA

A;Residues: 1-475 <ITO>

A;Cross-references: GB:M34551; NID:g337484; PIDN:AAA36581.1; PID:g337485

R;Chan, E.K.L.; Hamel, J.C.; Buyon, J.P.; Tan, E.M.

J. Clin. Invest. 87, 68-76, 1991

A;Title: Molecular definition and sequence motifs of the 52-kD component of human SS-A/Ro

A;Reference number: A37240; MUID:91086480; PMID:1985112

```

Db      6  LARRLOBEATSCICLOYFTDPVMTAGHNFCECIIQMSWEKGKGGKKGKSGFPCPEC 65
QY      54  RTTFAEPALAPSLKLANIVERSYSPFLDAILNARRAARPCOAH-DKVKLFCLTDRALLCF 112
Db      66  REMSPQRNLPRNLLTKVAEMARQHP--GLHKEDL---CQIHQEPKLCQDDDTPICV 119
QY     113  FCDPEPALHEQHQTVDGDADELORELKQLOALQDSEREHTALQLLKQO-LAETKSST 171
Db     120  VCREAQHRMHRVLPDDEAAREYKLRLEEDIKYLRE-EMMKETITLOAKESQITTEWQERV 178
QY     172  KSLRTTIGEAFERLHRLIRERQKAMLEEL---EADTARTITDIEQKVORYSQOLRKV--- 225
Db     179  KERRERLEEFQKVVFLVSEEPFLQLKKBEDDTLGLQDSKASLDHQSRSLDILLQ 238
QY     226  -----QEGAQIILQERLAETDRHTFLAGVASLSPERLKGKIHETMLTYDEPPTSXYT--G 276
Db     239  LEEQTQCEPLQMLQD-----VKDITLTKRESLSMQYPEVVL---PVAIKTVCRV 283
QY     277  PLOYTIWKSLFODLHPVPAAITLDPGTAHORLILSDDCITVAYGN-----LHPQLODSP 331
Db     284  PGQTEVLKSPQEDVVP-----DPSTAYPYLLL-----YESQRVYLSPPPEGAP 328
QY     332  ---KRFOVESVVLGSEAFSGGVHYWEV--VVAETQWVIGLAHEAAARKGSIQIQPSRGF 386
Db     329  YSKDRFLAYPCAVGCKGFSGRHYWEVGMNLTGTALMALGVCRDVWSEKDRVLKSPENG 388
QY     387  YCIYVMDGNQYSACIETPWTRNLNVEDKLDKGVGFVDYDQGLLIFYNADDMSLMYTFRE-KF 445
Db     389  WVWQLSGKGLPLPLNLSIPVLTLEPSPHMGIFLDFQAGEVSFVSVDNGSHLHFSQVAF 448
QY     446  PGKLCYSFPGQSHANGKNVQPLRINTV 473
Db     449  RGPILLPFECLG-SPKSGOMV-----ISTV 471

```

RESULT 8

ring finger protein.FXY - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C:Accession: T09482
R:Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A:Description: The human FXY maps to chromosome Xp22.3: Implications for evolution
A:Reference number: Z16687
A:Accession: T09482
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PER>
A:Cross-references: EMBL:AF035360; NID:g2827993; PID:g2827994
C:Genetics:
A:Gene: FXY
A:Map position: Xp22.3
C:Superfamily: RING finger homology
F:6-65/Domain: RING finger homology <RRN>

	Query Match	14.9%;	Score 372.5;	DB 2;	Length 667;	
	Best Local Similarity	21.6%;	Pred. No. 1.1e-15;			
	Matches 142;	Conservative	93;	Mismatches 199;	Indels 223;	Gaps 23
QY	4	SLKDLLCSICLSIQDPVSLGCEHYFCRC---	ITEHWVRQEAQ---	GARDCEPCR-	55	
	:	: :	: :	:	:	:
Dd	3	TLESLTCPLCLEFEDPELLUPCAHSLCNCNHRILVSHCATNESVESITAFQCCTCRHV	62			
QY	56	-TFAS--PALAPSLKANIANVERYS-----	SFFDLAINAR----	87		
	:	: :	: :	:	:	:
Dd	63	ITLSORGLDGLKRNTVLQNIDRFOKASVGSPNSPETERAFDANTWTSAEKVLCQFC	122			
QY	88	-----PAARP-----	CQAH--DK	98		
	:	: :	: :	:	:	:
Dd	123	DONBRADAKTCTWCVEVSNCYDEICKATPHNKPKPTGHRLLIEPIPSHSIRGLMCLBHEDEBK	182			

A,Accession: A37240
A,Molecule type: mRNA
A,Residues: 1-51,'A',53-475 <CHA>
A,Cross-references: GB:M62800; NID:G338489; PIDN:AAA36651.1; PID:G338490; GB:M35041
C,Genetics:
A,Gene: GDB:SSA1
A,Cross-references: GDB:133758; OMIM:109092
A,Map position: 11p15.5-11p15.5
A,Introns: 136/3; 168/3; 245/3; 253/2; 287/1
C,Superfamily: rfp transforming protein; RING finger homology
C,Keywords: DNA binding; nucleus; zinc finger
F,12-60/Domain: RING finger homology <RNG>
F,16-54/Region: zinc finger C3HC4 motif

Query Match 22.1%; Score 552.5; DB 1; Length 475;
Best Local Similarity 31.3%; Pred. No. 4.1e-27;
Matches 150; Conservative 88; Mismatches 208; Indels 33; Gaps 14;

Qy 7 DELLCSICLSIVODPVSIGCEHYFCRCITTEHWROAQAQDCPEGCRRTFAEPALAPSL 66
Db 12 BEVTCPICLDPFVEPSIECGHSFCQECISQ----VGKGGSVCFVCQRQRLKLNLRNR 67
Qy 67 KIANTVERYSFFPDAILNARRAARPCQAH-DKVKLFCLTDRLALCFCDPEPALHEQHV 125
Db 68 QIANVNNNLKETSQEA--REGTQGERCAVHGERLHLFCXDKGKALCWCAQSRKHDDHAM 125
Qy 126 TGIDAFDELQELKDQALQDSEHTEHALQI---LKPQLAETKSTKSRLRTTIGFAF 182
Db 126 VPLEEAQAQEQKIQVALGELR-RKQELAEKLEVEIAIKR--ADWKKTVETQKRIHAEF 182
Qy 183 EELHRLLEERQKAMLEELRADTARTLTDIEQKVORYSQQLRKVQEGAIQLERLAETDRH 242
Db 183 VOQKNFLVEEQKQQLQELKDEEQLRIKEAKLAQQ-----SQALQELISELDR 235

Db 236 CHSSALELLEQEVIIIVILERSGSMVKLDLIDITSPELRSVCHVPGGLKMLKTCVAVH-----IT 290
 QY 299 LDPGTAHQRLIILISDDCTIIVAYGNLHPLOLQDSPKRFDEVSVLGSEAFSSGVHYWEVVVA 358
 Db 291 LDPDTANPWLIIISDEDRRQVRLGDTQ-QSIPGNERFDSYPMVLGAQHPSHGKHYWEVDVT 349
 QY 359 EKTQWVIGLAHEAASKSGSIQIQPSRGFYCIVMHDGNQYSACTBPWTRLNVRDKLDKGVV 418
 Db 350 GKEMDLGVCRDSVRRRGHLLSKSGFWIWLWNKQKYEACTYPTQPLHLQVPCQVGI 409
 QY 419 FLDYDQGLLIFYN-ADMSWLYTFRE-KFGPKLCSYFSPGQSHANGKXVQPLRINTVRI 475
 Db 410 FLDYEAGMVSFYNIITDGHSLIYSFSECAFTGPLRPFSPG-FNDGGKNTAPLTLOPLNI 467

RESULT 7
 JE0343
 terf protein - rat
 C/Species: Rattus norvegicus (Norway rat)

C/Accession: JE0343
 R/Ogawa, S.; Goto, W.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramatsu, M.; Inoue, S.
 Biochem. Biophys. Res. Commun. 251, 515-519, 1998
 A>Title: Molecular cloning of a novel RING finger-B box-coiled coil (RBCC) protein, termed
 A:Reference number: JE0343; MUID:99011410; PMID:9792805
 A:Accession: JE0343
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-477 <OGA>
 C:Superfamily: rfp transforming protein; RING finger homology
 F,12-71/Domain: RING finger homology <RRN>
 Query Match 18.9% Score 472.5; DB 2; Length 477;
 Best Local Similarity 28.9%; Pred. No. 4e-22;
 Matches 147; Conservative 81; Mismatches 203; Indels 77; Gaps 19;


```
QY 99 VKLFCLTDRALCFDCEPALHEQHCVTGIDDAFDELORELKQLOAL--QDSEREHTEA 156
Db 183 VNMVCTDDQLICALCKLVGRHRDQVAALSERYDKLQNLNLTNLKRNTELETLIA 242
QY 157 LQLLKQRLAETKSSKSLRTTIGEAFLRLRLRERQKAMLEELADTARTLTIDIEQKVQ 216
Db 243 KLIQTQCHVEVNASRQEAHLT--EEDCLLIEIIQORRQIIGTKIKEGKVMRLKLAQOIA 300
QY 217 RYSOQLRKVOEGAQILQERLAETDRHTFLAGVASLSERL-----KGKIHTNL--TYE 267
Db 301 NCKQCIERSASLISOAHSKENDHARFLQTAKNITERVSMATASSQVLIPEINLNDTFD 360
QY 268 ----DFPTSK-----YTGP-----KSLFQDIHPVPA-- 420
Db 361 TFALDFSREKKLLECLDYLTAFPNPTIREELCTASYDTITVHWTSDDFSVSVELQYTI 420
QY 283 ----W-----KSLFQDIHPVPA-- 296
Db 421 FTGQANVSVLCSNADSMWIVPNIKQNHVTVHGLQSGTKYIFMWKAINQAGSRSSBPGLK 480
QY 297 ----LTLDPGTAHORLILSDDCITIVAGNLHPQPLQDS-----PKRFDVEVS--VLGS 343
Db 481 TNSQPFKLDPKSAHKLKVSHD-----NLTVRDESSSKSHPTPERFTSQSGYGVAGN 533
QY 344 EAFSGVHYWEVVAEKTQWVIGLAHEAASRKGSIQIQRSGFYC-----IVMHDGNQY 397
Db 534 VFIDSGRHYWEVVSIGSTWYALGAYKAPKHEWIGKNSAWALCRNNWVVRHNSKEI 593
QY 398 SACTEPWTRLNVRKLDKGVFLDYDQGLLIIFYNADMSWLYTFREKFPGLKCSYFS 454
Db 594 PIEPAPHLR-----RVGILLDYNGSIAFYDALNSIHLYTFDVAFAQVPCVTF 642

RESULT 9
T12494
hypothetical protein DKFZp434C091.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Sep-1999
C:Accession: T12494
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17525
A:Accession: T12494
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <POU>
A:Cross-references: EMBL:AL080170
A:Experimental source: adult testis; clone DKFZp434C091
C:Genetics:
A:Note: DKFZp434C091.1
C:Superfamily: rfp transforming protein; RING finger homology

Query Match 14.8%; Score 370.5; DB 2; Length 438;
Best Local Similarity 30.2%; Pred. No. 8.3e-16;
Matches 105; Conservative 56; Mismatches 140; Indels 47; Gaps 9;

QY 126 TGIDDAFDELORELKQLOALQDLSERHTEALQLLKLQ--ARTKSTKSLRTTIGE-- 180
Db 80 SGALGAADWLAVQVKLQ-- 127
QY 181 -----AFERHLRLRERQKAMLEELPADTARTLTIDIEQVQRYSOQLRKVOEGAQI 231
Db 128 EMORQFRLEFEKHGFLAQEQQLRLEAEERATLQRLRESKSLRVQOSKALKELADE 187
QY 232 LQERLAETDRHTFLAGVASLSERLKGKIHTNLTYEDFPPTSKYTG---PLOYTIWKSFLQ 288
Db 188 LQER-CORPALGLEGVRGVLSRKA---VTRLEAENIPMELKTACCIPGRRELLRKFQV 243
QY 289 DIHPVPAALTLDPGTAHORLILSDDCITIVAGNLHPQPLQD---SPKRFDEVSVLGSEA 345
Db 244 DV-----KLDPAHAHPSLLLTADLSRVQDQ-----EPMDVFNPNRPFDTWPCILGLQS 292
QY 346 FSSGVHYWEVVAEKTQWVIGLAHEAASRKGSIQIQRSGFYCIVMHDGNQYSACTEPWT 405
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```
Db 293 FSSGRHYEVLVGEAEWGLGVCQDTLPRKGTMPSPENGWALMLLKGYMWLASPSV 352
QY 406 RLNVDRKLDKGVFLDYDQGLLIIFYNADMSWLYTFREKFPGLKCSYF 453
Db 353 PLQLQESPRCIGFLDYEAEGISFNVTGSGYIYTFNQLFSGLLRPYF 400

RESULT 10
T09013
RING finger protein Fxy - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Sep-2000
C:Accession: T09013
R:Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A:Title: A gene spans the pseudautosomal boundary in mice.
A:Reference number: Z16531; MUID:98004518; PMID:9342357
A:Accession: T09013
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PAL>
A:Cross-references: EMBL:AF026565; NID:g2589222; PIDN:AAB81986.1; PID:g2589223
C:Genetics:
A:Gene: Fxy
A:Map position: X; Y
C:Superfamily: RING finger homology
C:Keywords: zinc finger
F:6-65/Domain: RING finger homology <RNN>

Query Match 14.6%; Score 364.5; DB 2; Length 667;
Best Local Similarity 21.8%; Pred. No. 3.4e-15;
Matches 143; Conservative 87; Mismatches 204; Indels 223; Gaps 23;

QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRR-----ITEHWVRQ---BAQAGADCPECR- 55
Db 3 TLESELTCPICLELFEDPDLPLPCAHSCLFCNCAHRLVSHCATNPVPSINAFQCPTCRHV 62
QY 56 -TFAB---PALAPSLKLANIVERYS-----SPDLAILNAR----- 87
Db 63 ITLSQRLGDLGKRNVTQLNIIDRFQKASVSGPNSPSTRERRAFDANTMSAEKVLQCF 122
QY 88 -----RAARP-----COAH--DK 98
Db 123 DQPAQDAVKTCVTCEVSYCDECLKATHPNKPFTHRLIEPIPDSHIRGLTCLHEDEK 182
QY 99 VKLFCLTDRALCFDCEPALHEQHCVTGIDDAFDELORELKQLOAL--QDSEREHTEA 156
Db 183 VNMVCTDDQLICALCKLVGRHRDQVAALSERYDKLQNLNLTNLKRNTELETLIA 242
QY 157 LQLLKQRLAETKSSKSLRTTIGEAFLRLRLRERQKAMLEELADTARTLTIDIEQKVQ 216
Db 243 KLIQTQCHVEVNASRQEAHLT--EEDCLLIEIIQORRQIIGTKIKEGKVIKRLKLAQOIA 300
QY 217 RYSOQLRKVOEGAQILQERLAETDRHTFLAGVASLSERL-----KGKIHTNL--TYE 267
Db 301 NCKQCIERSASLISOAHSKENDHARFLQTAKNITERVSMATASSQVLIPEINLNDTFD 360
QY 268 ----DFPTSK-----YTGP-----KSLFQDIHPVPA-- 420
Db 361 TFALDFSREKKLLECLDYLTAFPNPTIREELCTASYDTITVHWTSEDFSVSVELQYTI 420
QY 283 ----W-----KSLFQDIHPVPA-- 296
Db 421 FTGQANVSVLCSNADSMWIVPNIKQNHVTVHGLQSGTKYIFTVKAINQAGSRSSBPGLK 480
QY 297 ----LTLDPGTAHORLILSDDCITIVAGNLHPQPLQDS-----PKRFDVEVS--VLGS 343
Db 481 TNSQPFKLDPKSAHKLKVSHD-----NLTVRDESSSKSHPTPERFAGQSGYGVAGN 533
QY 344 EAFSGVHYWEVVAEKTQWVIGLAHEAASRKGSIQIQRSGFYC-----IVMHDGNQY 397
Db 534 VFIDSGRHYWEVVSIGSTWYALGAYKAPKHEWIGKNSAWALCRCHNHVVRHHDGKET 593
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QY 398 SACTETWTLNVRDKLVGVFLDYDQGLLIFYNADMSWLYTFRKFPCKLCSYFS 454

Db 461 CLWSS---GK--KPLTI 472

Search completed: July 23, 2004, 15:08:32
Job time : 19 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:04:20 ; Search time 13 Seconds
(without alignments)
1902.563 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELLCSICLSIQD.....GSHANGKNVQLRINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	772	30.8	624	1	A33_PLEWA	Q02084 pleurodeles
2	663.5	26.5	518	1	RN23_HUMAN	Q9hcm9 homo sapien
3	655.5	26.2	488	1	RN23_MOUSE	Q9esn2 mus musculu
4	583	23.3	513	1	RFP_HUMAN	P14373 homo sapien
5	580	23.2	522	1	RFP_MOUSE	Q62158 mus musculu
6	560	22.4	468	1	TM11_HUMAN	Q96f44 homo sapien
7	554.5	22.1	467	1	TM11_MOUSE	Q99pq2 mus musculu
8	552.5	22.1	475	1	R052_HUMAN	P19474 homo sapien
9	550.5	22.0	511	1	TRM7_HUMAN	Q9c029 homo sapien
10	528	21.1	470	1	R052_MOUSE	Q62191 mus musculu
11	505.5	20.2	488	1	TRM6_HUMAN	Q9c030 homo sapien
12	489	19.5	465	1	RN15_HUMAN	Q00635 homo sapien
13	486	19.4	477	1	TM17_MOUSE	Q7lpm3 mus musculu
14	475.5	19.0	477	1	TM17_RAT	Q9wv59 rattus norv
15	459	18.3	477	1	TM17_HUMAN	Q9y577 homo sapien
16	456	18.2	489	1	RNF9_MOUSE	Q9wh5 mus musculu
17	449.5	18.0	482	1	RNF9_HUMAN	Q9uhy6 homo sapien
18	449	17.9	539	1	Z173_HUMAN	Q12899 homo sapien
19	448	17.9	539	1	Z173_PANTR	Q7yr34 pan troglod
20	444	17.7	481	1	RNF9_PANTR	Q7yr32 pan troglod
21	439	17.5	461	1	TM15_PIG	Q9tsw0 sus scrofa
22	430	17.2	465	1	TM15_HUMAN	Q9c019 homo sapien
23	428	17.1	465	1	TM15_PANTR	Q7yr33 pan troglod
24	427.5	17.1	781	1	MEFV_HUMAN	O15553 homo sapien
25	410.5	16.4	496	1	TM30_MOUSE	P15533 mus musculu
26	408.5	16.3	493	1	TRM5_HUMAN	Q9c035 homo sapien
27	372.5	14.9	667	1	MID1_HUMAN	O15344 homo sapien
28	369.5	14.8	667	1	MID1_RAT	P82458 rattus norv
29	362	14.5	680	1	MID1_MOUSE	Q70583 mus musculu
30	360.5	14.4	667	1	MID1_MUSSP	P82457 mus sprcet
31	341	13.6	630	1	Z147_HUMAN	Q14258 homo sapien
32	340.5	13.6	685	1	MID2_MOUSE	Q9qus6 mus musculu
33	326.5	13.0	715	1	MID2_HUMAN	Q9ujv3 homo sapien

34	321.5	12.8	442	1	TM14_HUMAN	Q14142 homo sapien
35	306	12.2	288	1	RFL1_HUMAN	O75677 homo sapien
36	304.5	12.2	634	1	Z147_MOUSE	Q61510 mus musculu
37	301.5	12.0	526	1	BUTY_BOVIN	P18992 bos taurus
38	297.5	11.9	524	1	BUTY_MOUSE	O62556 mus musculu
39	296	11.8	288	1	RFL2_HUMAN	O75678 homo sapien
40	295	11.8	288	1	RFL3_HUMAN	O75679 homo sapien
41	293	11.7	526	1	BUTY_HUMAN	Q13410 homo sapien
42	279.5	11.2	452	1	RN18_HUMAN	Q9ns80 homo sapien
43	276	11.0	425	1	TM31_HUMAN	Q9bzy9 homo sapien
44	269	10.7	551	1	RN27_MOUSE	Q99pj2 mus musculu
45	267	10.7	551	1	RN27_HUMAN	Q9bzy9 homo sapien

ALIGNMENTS

RESULT 1
A33_PLEWA
ID_ A33_PLEWA STANDARD; PRT; 624 AA.
AC Q02084;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc-binding protein A33.
OS Pleurodeles waltlii (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae;
OC Pleurodeles.
OX NCBI_TaxID=83119;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=93154311; PubMed=7679068;
RA Bellini M., Lacroix J.-C., Gall J.-G.;
RT "A putative zinc-binding protein on lampbrush chromosome loops.";
RL EMBO J. 12:107-114(1993).
CC -!- FUNCTION: May be a nuclear regulatory protein that is stored
CC in the germinal vesicle for use during early embryogenesis
CC and may play a role in the synthesis or processing of pre-mRNA
CC during oogenesis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: It first appears on the chromosome loops
CC and in the nucleoplasm of the germinal vesicle (GV). It is
CC transmitted to the egg at GV breakdown and appears in embryonic
CC nuclei at the mid-blastula stage and is found in many but not
CC all nuclei at still later stages of embryogenesis.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 B box-type zinc finger.
CC -!- SIMILARITY: Contains 1 SPY domain.

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or send an email to license@isb-sib.ch).

EMBL; L04190; AAA49614.1; -;
PIR; S28418; S28418.
InterPro; IPR001870; B302.
InterPro; IPR003649; Bbox_C.
InterPro; IPR006574; PRY.
InterPro; IPR003877; SPY receptor.
InterPro; IPR000315; Znf.Bbox.
InterPro; IPR001841; Znf_ring.
Pfam; PF00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00502; BBC; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00589; PRY; 1.

MEDLINE=20462913; PubMed=11006080.

RX Orimo A., Yamagishi T., Tominga N., Yamauchi Y., Hishinuma T.,
RA Okada K., Suzuki M., Sato M., Nogai Y., Suzuki H., Inoue S.,
RA Yoshimura K., Shimizu Y., Muramatsu M.;
RT "Molecular cloning of testis-abundant finger protein/ring finger
protein 23 (RNF23), a novel RING-B box-coiled coil-B30.2 protein on
the class I region of the human MHC";
RT Biochem. Biophys. Res. Commun. 275:45-51(2000).
[2]

SEQUENCE FROM N.A. (ISOFORM 2).

RP TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
RA Raha S.S., Loquellano P.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibes R.A.
FAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=1;
Isoid-Q9HGM9-1; Sequence=Displayed;
Name=2;
Isoid-Q9HGM9-2; Sequence=YSP_005755;
Note-No experimental confirmation available;
CC -I- TISSUE SPECIFICITY: Ubiquitous; highly expressed in testis.
CC -I- SIMILARITY: Contains 1 RING-type zinc finger.
CC -I- SIMILARITY: Contains 1 B box-type zinc finger.
CC -I- SIMILARITY: Contains 1 SPRY domain.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; AB046381; BAB16374.1; -;
DR EMBL; BC007661; AA07661.1; -;
DR PIR; JC7387; JC7387.
DR HSSP; P15919; IRMD.
DR GENE; HGNC:10085; TRIM39.
MIN; 605700; -;
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; ZnfxBox.
DR InterPro; IPR001841; ZnfxRing.
PFAM; PF00622; SPRY; 1.
PFAM; PF00643; zf-B_box; 1.
PFAM; PF00097; zf-C3HC4; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00589; PRY; 1.
SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PS50119; ZF-BBOX; 1.
PROSITE; PS00518; ZF-RING; 1.
PROSITE; PS50089; ZF-RING; 1.
PROSITE; PS50089; ZF-RING; 1.


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DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; Zf-B_Box; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00589; PRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS00119; ZF_BBOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Zinc-finger; Antigen- RNA-binding; Ribonucleoprotein; DNA-binding.
FT ZN_FING 20 59 RING-TYPE.
FT ZN_FING 96 127 B_BOX-TYPE.
FT DOMAIN 215 236 LEUCINE-ZIPPER.
SQ SEQUENCE 470 AA; 54175 MW; 393AESA5FD254855B CRC64;

Query Match 21.1%; Score 528; DB 1; Length 470;
Best Local Similarity 29.7%; Pred. No. 1.1e-23;
Matches 146; Conservative 87; Mismatches 189; Indels 70; Gaps 18;

QY 7 DELLCSICLSIYQDPVSLGCHYFCRCRITTEHWVQEAQAGARDPCPCRTFAEPALAPSL 66
DB 16 EEWTCISICLDPWVPEMSIEGCHFCFCEIFE---VGKNGSGSCPCCQOQLRLNLRPNR 71
QY 67 KLANIVERYSSPFLDAILNARRARP--COAH-DKVKLFCLTDRALLCFCEBPALHEQH 123
DB 72 HIANMVENLKQI-----AONTKKSOTHCWKGKHLFCFEDGQALCWCAQSGKGRDH 127
QY 124 QVTGIDDAFDELQELKQALQALQDSERHEHTALQL-LKRLAETKSKTSKIRTTTIGFAF 182
DB 128 TRVPEEAAKVQEKHVVLEKLRKG-KELAEKEMDLTWQTDWGRNIDTQKSRHAEF 186
QY 183 ERIHLRLREROKAMLELEADTARTLTIDIEQVQRYSQLRKVOEGAQILOERLAETDRH 242
DB 187 ALQNSLLAQEQQLQLEKQDREYLRLLGKKE-----AELAKNQALQELISELER- 238
QY 243 TFLAGVASLSRLKKG-----IHTNLTPE-----DPFTSKYTG- 280
DB 239 -----RIGSELELLQEVRIILERSGSGWNLDITDIDAPDLTSTCPVGRKKMLR 287
QY 281 TIWKSFLQDHPVPAALTDPGTAHQRLILSDCTTIVAGNLHPQLQSPKRFDEVSU 340
DB 288 TW-----VH-----ITLDNTANSWLLISKDRQVRMGDTH-QNVSDNKERFSNPMV 335
QY 341 LGSEAFSSGVHVVVVAEKTOVIGLAHEAASRKSGIQIPGRGYCIVMHDGNOYSAC 400
DB 336 LGAQRFSSGKMYWEVDVTKAEMDLGVCRDSVQKGFSLSPENGFWTIWLQ-DSYEA 394
QY 401 TEPWTLNVRDLKDKGVFLDYDQGLLIIFYN-ADDMSNLYTFPE-KFPGKLCYSFPGQS 458
DB 395 TSPQTTLHTQVPPCIGIFVDYEAQVVSFYNTIDHGSLIYTFSECFVAGLRPFNVGN 454
QY 459 HANGKNVQPLRI 470
DB 455 YSGG-NAAPLKL 465

RESULT 11
ID TRM6_HUMAN STANDARD; PRT; 488 AA.
AC Q9C030;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tripartite motif protein 6.
GN TRIM6.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```



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Db 179 ERCLQTFNQRLNDRVQREKLEQBEKKGRIIEEAENDLVHQTQSLRELISDL- 237
Qy 234 ERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDFTSKYTGLPQYTIWKSLEFQ- 288
Db 238 ERRCQGSTMEILLQDVSDYTER-----SEFWTLRKPEALP-TKLRSMPFRAPDLK 284
Qy 289 -----DIHFVPAALTLDPGTAHORLLISDCTTIVAGNHLHPQLQSPKRFQVEV 338
Db 285 RMLRVCRELTQVQSWVDVTLNPHPTANLNLAKNRQVRVFGAKVSPGSCLEKHYD--C 342
Qy 339 SVLGSEAFSSGVHYWEVVAEKTOWVIGLA-----HEAASRKGSIQIOPSRGEY 387
Db 343 SVLGSEAFSSGVHYWEVVAEKTOWVIGLA-----HEAASRKGSIQIOPSRGEY 402
Qy 388 CIVMHGNGQYAC--TEPTWRLNVRDKLVKGVFLDYDQGLLIIFYNADMSW-LYTF-RE 443
Db 403 VIGLQNHXYRAYEDSSPLLISMTVPPRRVGVFLDYEAGTVSFYNTVNHGFPFIYTFSKY 462
Qy 444 KFPGLKCSYFSP 455
Db 463 YFPTTLCYFNP 474

RESULT 12
RN15_HUMAN
ID RN15_HUMAN STANDARD; PRT; 465 AA.
AC O00635;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RING finger protein 15 (Zinc finger protein Rofet) (Tripartite motif-
DE containing protein 38).
GN TRIM38 OR RNFI5 OR RORET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mamalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=97294057; PubMed=9149941;
RA Ruddy D.A., Krommal G.S., Lee V.K., Mintier G.A., Quintana L.,
RA Domingo R. Jr., Meyer N.C., Irinko A., McClelland E.E., Fullan A.,
RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,
RA Wolff R.K., Schatzman R.C., Feder J.N.;
RA "A 1.1-Mb transcript map of the hereditary hemochromatosis locus.";
RT Genome Res. 7:441-456(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -!- SIMILARITY: Contains 1 B box-type zinc finger.
CC -!- SIMILARITY: Contains 1 SPRY domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U91328; AAB82084.1; -.
CC EMBL; U90547; AAB53425.1; -.
CC EMBL; BC026930; AAB26930.1; -.
CC Genew; HGNC:10059; TRIM38.
CC InterPro; IPR001870; B302.
CC InterPro; IPR006574; PRY.
CC InterPro; IPR003877; SPRY receptor.
CC InterPro; IPR000315; Znf_Box.
CC InterPro; IPR001841; Znf_Ring.
CC Pfam; PF00622; SPRY; 1.
CC Pfam; PF00643; zf-B_box; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC PRINTS; PR01406; BBOXZNFINGER.
CC SMART; SM00336; BBOX; 1.
CC SMART; SM00589; PRY; 1.
CC SMART; SM00184; RING; 1.
CC SMART; SM00449; SPRY; 1.
CC PROSITE; PS01119; ZF_BBOX; 1.
CC PROSITE; PS00518; ZF_RING_1; 1.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC Zinc-finger; Polymorphism.
FT ZN_FING 16 63 RING-TYPE.
FT ZN_FING 88 129 B_BOX-TYPE.
FT DOMAIN 344 464 SPRY.
FT VARIANT 421 421 /FTID=VAR_013513.
FT CONFLICT 23 23 M -> I (IN REF. 2).
FT SEQUENCE 465 AA; 53416 MW; 30A884051A2DA058 CRC64;
Qy Query Match 19.5%; Score 489; DB 1; Length 465;
Best Local Similarity 29.3%; Pred. No. 2e-21;
Matches 137; Conservative 79; Mismatches 207; Indels 44; Gaps 11;
Qy 5 LKDELLSICLSIYQDPVSLGCEHYFPCRCITTEHWROEAGQARD----CEECRTFRBP 60
Db 10 MMEATCSICLSLMTNPFVINCCHSYCHLCITDFFKPNSQQLRQETECPCQCRPFHMD 69
Qy 61 ALAPSLKLANIVERYSSPPLDAILNARRAAPCOAH-DKVKLFCLTDRLALCFCEDEPAL 119
Db 70 SLRPNKQLGSLIE-----ALKETDQMSCEHGEQFHLFCEDEQLICWRCEAPQ 120
Qy 120 HEQHQVTGIDDAFDELORELKDQALQDSREHTEALQLKRLQLAETKSTKSLRTTIG 179
Db 121 HKGHTTALVEDVCQYKELQKAVTKLQLEDRCQKLEDRQKLEAMRTTKWKEVQIQKIR 180
Qy 180 EAFELHRLEROKAMLELEADARTLT---DIEKVQVRSQQLR-----KVQEG 228
Db 181 SDFKNQLQCFLEHEEKSLWLRLEKEEQQLTSLRDYEAGLGLKSNELKSHILEBEKCGS 240
Qy 229 AQILOERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDFTSKYTGLPQYTIWKSLEFQ 288
Db 241 AQKLLQNVNDT-----LSRSWAVKLETSEAVSLELHTWCNVSPLYFDVKKMLRS 289
Qy 289 DIHPVPAALTLDPGTAHORLLISDCTTIVAGNHLHPQLQD-SPKRFQVSVLGSSEAFS 347
Db 290 --HQV--SVTLDPDTAHELILSEDRRQVTRG--YTQENQDTSRRRTAFPCVLGCEGT 343
Qy 348 SCVHYWEVVAEKTQWVIGLAHEAASRKGSIQIOPSRGFYCIYVMDGNQYACTEPTWRL 407
Db 344 SGRIFYEVDVGEGTGWDLVGCMENVGRTGKMQPQSGFQWTLRLCKKGYVALTSPTSL 403
Qy 408 NVRDKLDKGVFLDYDQGLLIIFYNADMSWLYTF-REKFPGLKCSYF 453
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DR EMBL; AF156271; AAD40286.1; -;
DR EMBL; EC033788; AAH33788.1; -;
DR Genew; HGNC:13430; TRIM17.
DR MIM; 606123; -;
DR InterPro; IPR001870; B302.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS00119; ZF_BOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Coiled coil; Zinc-finger.
FT ZN_FING 16 66 RING-TYPE.
FT ZN_FING 94 135 B_BOX-TYPE.
FT DOMAIN 135 223 COILED COIL (POTENTIAL).
FT DOMAIN 297 456 B30.2-LIKE.
SQ SEQUENCE 477 AA; 54418 MW; ECA4010661ADD28A CRC64;

Query Match 18.3%; Score 459; DB 1; Length 477;
Best Local Similarity 27.0%; Pred. No. 1.1e-19;
Matches 130; Conservative 85; Mismatches 214; Indels 52; Gaps 12;

QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWV-----RQEAQAGDCPEC 53
Db LARKIQEATCSICLDYFDPTWTTCTGHNFCACQLSWEKARGKGRKRKSGFPCEC 65

QY 54 RTFAEPALAPSLKLANIVERYSSFPDLAINARARPCQA-HDKVKLFCLTDRALLCF 112
Db REMSPQNLPLNLLTKVAEMAQHP-----GLOKQDLCOEHPELKLFCQKQSPICV 119

QY 113 FCEPALHEQOVTGIDDAFDELQRELQALQDSEREHTEALQLKRO-LAETKST 171
Db VCRESEHRLHRLVPAEEAVQGYKLLEEDMEYLRE-QITRTGNLQARBEQSLAEWQGV 178

QY 172 KSLRTTIGAFERLHLEROKAMLELEADTARTLTLDIEQV-----QRYSQQLRKVQ 226
Db KERRERIVLEFKMNLVLEEQRLLQALETEETASRLRESVACLDRQHSLELLIQ 238

QY 227 EGAQIIQERLAETDRHTFLAGVASLSERLKGKHETNLTYEDFPSTKYTGPIQYTIWKS 286
Db -----LEERSTQGLQMLQDMKEPLSRKNVSVQCEVAPPTPRVCRVPGQIEVLGRF 293

QY 287 FQDIHPVPAALHLDGTAHQRLILSDDCITVAYGNLHPQLQDSPK-----RPDVEV 338
Db LEDVVP-----DATSAYPYLL-----YESRRYLGSSPEGSGFCSKDRFVAYP 338

QY 339 SVLGSEAFSSGVHYWEV--VVAEKTOWITGLAHEAASRKSGSIQIPSRGFYCIWMHDG 396
Db CAVGQTAFSSGRHYVEVGNNITGDALWALGVCRDNRKDRVPKCPENGFWVQISKGT 398

QY 397 YSACTEPWTRLNVRDKLDKGVFLDYDQGLLIIFYNADDMSWLYTFRE-KPPGKLCSYFSP 455
Db YLSTFSALTTPVMLMEPPSHMGIFLDFEAGEVSFYSVSDGSHLHTYSQATFPGLQPF 458

QY 456 G 456
Db 459 G 459

Search completed: July 23, 2004, 15:08:04
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:03:50 ; Search time 42 Seconds
(without alignments)
3568.361 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELICSLSIYQD.....GQSHANGKNVQPLINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25; *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirois: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2504	100.0	475	4	Q9BVG3	Q9bv93 homo sapien
2	2491	99.5	475	4	Q9NVG0	Q9nv90 homo sapien
3	2491	99.5	475	11	Q8OV85	Q8ov85 mus musculus
4	763.5	30.5	609	13	Q92021	Q92021 xenopus lae
5	748.5	29.9	610	13	Q91431	Q91431 xenopus lae
6	693.5	27.7	453	13	Q801R9	Q801r9 xenopus lae
7	664.5	26.5	496	11	Q8K0F7	Q8k0f7 mus musculus
8	662.5	26.5	488	4	Q81YT9	Q81yt9 homo sapien
9	638.5	25.5	479	13	Q7ZU70	Q7zu70 brachydanio
10	619	24.7	500	4	Q86WT6	Q86wt6 homo sapien
11	603.5	24.1	500	11	Q80X56	Q80x56 mus musculus
12	593.5	23.9	500	11	Q8VHZ6	Q8vhz6 mus musculus
13	593	23.7	483	11	Q81012	Q81012 mus musculus
14	588	23.5	483	11	Q81011	Q81011 rattus norv
15	581	23.2	486	6	Q865W2	Q865w2 sus scrofa
16	577	23.0	513	11	Q8C2Q5	Q8c2q5 mus musculus

17	576	23.0	486	4	Q86XT3	Q86xt3 homo sapien
18	576	23.0	513	11	Q99LK1	Q99lk1 mus musculus
19	575.5	23.0	487	4	Q86XT4	Q86xt4 homo sapien
20	572	22.8	506	11	Q62157	Q62157 mus musculus
21	553.5	22.1	483	11	Q8VDX5	Q8vdx5 mus musculus
22	550.5	22.0	485	4	Q96PF7	Q96pf7 homo sapien
23	550.5	22.0	485	4	Q8WZ70	Q8wz70 homo sapien
24	550.5	22.0	511	4	Q96J90	Q96j90 homo sapien
25	540.5	21.6	469	6	Q7YRV4	Q7yrv4 bos taurus
26	529	21.1	470	11	Q921V6	Q921v6 mus musculus
27	523.5	20.9	485	11	Q8K243	Q8k243 mus musculus
28	520	20.8	501	11	Q8BVV9	Q8bvv9 mus musculus
29	520	20.8	501	11	Q8VID4	Q8vid4 mus musculus
30	520	20.8	514	11	Q810V7	Q810v7 mus musculus
31	520	20.8	516	11	Q8C006	Q8c006 mus musculus
32	516	20.6	486	11	Q7TQL7	Q7tql7 mus musculus
33	513	20.5	470	11	Q8BVP1	Q8bvp1 mus musculus
34	505.5	20.2	516	4	Q86WZ8	Q86wz8 homo sapien
35	501	20.0	471	4	Q8NA35	Q8na35 homo sapien
36	500	20.0	468	4	Q8N9V2	Q8n9v2 homo sapien
37	494	19.7	514	13	Q800L5	Q800l5 anguilla ja
38	486	19.4	477	11	Q7TEM3	Q7tpm3 mus musculus
39	483	19.3	493	4	Q86XQ0	Q86xq0 homo sapien
40	483	19.3	504	4	Q9UPQ4	Q9upq4 homo sapien
41	480.5	19.2	341	4	Q81YX3	Q81yy3 homo sapien
42	475.5	19.0	477	11	Q9WV59	Q9wv59 rattus norv
43	459	18.3	477	4	Q9Y577	Q9y577 homo sapien
44	458.5	18.3	296	4	Q8WY17	Q8wyl7 homo sapien
45	456	18.2	489	11	Q80WA9	Q80wa9 mus musculus

ALIGNMENTS

RESULT 1

Q9BVG3					
ID	Q9BVG3	PRELIMINARY;	PRT;	475	AA.
AC	Q9BVG3;				
DT	01-JUN-2001 (TrEMBLrel. 17, Created)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Eye;				
RA	Strausberg R.;				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
CC	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.				
DR	EMBL; BC001222; AAH01222.1; -				
DR	EMBL; BC012152; AAHL2152.1; -				
DR	EMBL; BC007999; AAH07999.1; -				
DR	EMBL; BC011689; AAHL1689.1; -				
DR	GO; GO:0005622; C:intracellular; IEA.				
DR	GO; GO:0008270; F:zinc ion binding; IEA.				
DR	InterPro; IPR001870; B302.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR006574; PRY.				
DR	InterPro; IPR003877; SPKX_receptor.				
DR	InterPro; IPR000315; Znf_Box.				
DR	Pfam; PF00622; SPRY; 1.				
DR	Pfam; PF00643; zf-B_box; 1.				
DR	Pfam; PF00097; zf-C3HC4; 1.				
DR	SMART; SM00589; PRY; 1.				
DR	SMART; SM00184; RING; 1.				
DR	PROSITE; PS00290; IG_MHC; 1.				
DR	PROSITE; PS00119; ZF_BOX; 1.				
DR	PROSITE; PS00518; ZF_RING_1; 1.				
DR	PROSITE; PS00089; ZF_RING_2; 1.				

KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 475 AA; 54267 MW; DC15CA9B795DEBB0 CRC64;

Query Match 100.0%; Score 2504; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.1e-160;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQAGARDCEPCRRTFABP 60
DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQAGARDCEPCRRTFABP 60
QY 61 ALAPSLKLANIYVERYSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFDCDEPALH 120
DB 61 ALAPSLKLANIYVERYSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFDCDEPALH 120
QY 121 EQHVTGIDDADELORELKDQLOALQDSERHEALQLLKRQLAETKSTSLRTTIGE 180
DB 121 EQHVTGIDDADELORELKDQLOALQDSERHEALQLLKRQLAETKSTSLRTTIGE 180
QY 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQOLRKVOEGAIQLQERLAETD 240
DB 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQOLRKVOEGAIQLQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDPPTSKYTGPLQYTIWKSFLQDHPVPAALTLD 300
DB 241 RHTFLAGVASLSERLKGKIHETNLTYEDPPTSKYTGPLQYTIWKSFLQDHPVPAALTLD 300
QY 301 PGTAFQRLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
DB 301 PGTAFQRLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
QY 361 TQWVIGLAHEAASRKGSIQIQSRGFYCIWMDGNQYSACTEPWTLNVRDLKDKVGVEL 420
DB 361 TQWVIGLAHEAASRKGSIQIQSRGFYCIWMDGNQYSACTEPWTLNVRDLKDKVGVEL 420
QY 421 DYDQGLLIIFYNADMSWLYTFREKPFKGLCSYFSPGQSHANGKNVQPLRINTVRI 475
DB 421 DYDQGLLIIFYNADMSWLYTFREKPFKGLCSYFSPGQSHANGKNVQPLRINTVRI 475

RESULT 2

Q9NVG0 PRELIMINARY; PRT; 475 AA.
AC Q9NVG0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ10759.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuko Y., Kanehori K.;
RT "NEO human cDNA sequencing project";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AK001621; BAA91792.1; -!
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; Zf-B_box; 1.

DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 475 AA; 54190 MW; 7C04489D3B5C0F6C CRC64;

Query Match 99.5%; Score 2491; DB 4; Length 475;
Best Local Similarity 99.6%; Pred. No. 8.4e-160;
Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQAGARDCEPCRRTFABP 60
DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQAGARDCEPCRRTFABP 60
QY 61 ALAPSLKLANIYVERYSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFDCDEPALH 120
DB 61 ALAPSLKLANIYVERYSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFDCDEPALH 120
QY 121 EQHVTGIDDADELORELKDQLOALQDSERHEALQLLKRQLAETKSTSLRTTIGE 180
DB 121 EQHVTGIDDADELORELKDQLOALQDSERHEALQLLKRQLAETKSTSLRTTIGE 180
QY 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQOLRKVOEGAIQLQERLAETD 240
DB 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQOLRKVOEGAIQLQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDPPTSKYTGPLQYTIWKSFLQDHPVPAALTLD 300
DB 241 RHTFLAGVASLSERLKGKIHETNLTYEDPPTSKYTGPLQYTIWKSFLQDHPVPAALTLD 300
QY 301 PGTAFQRLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
DB 301 PGTAFQRLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
QY 361 TQWVIGLAHEAASRKGSIQIQSRGFYCIWMDGNQYSACTEPWTLNVRDLKDKVGVEL 420
DB 361 TQWVIGLAHEAASRKGSIQIQSRGFYCIWMDGNQYSACTEPWTLNVRDLKDKVGVEL 420
QY 421 DYDQGLLIIFYNADMSWLYTFREKPFKGLCSYFSPGQSHANGKNVQPLRINTVRI 475
DB 421 DYDQGLLIIFYNADMSWLYTFREKPFKGLCSYFSPGQSHANGKNVQPLRINTVRI 475

RESULT 3

Q8OV85 PRELIMINARY; PRT; 475 AA.
AC Q8OV85;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN cDNA 6330414G21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA	Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RC	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6;
RA	Strausberg R.;
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC049095; AAH49095.1; -
DR	GO; GO:0005622; C:intracellular; IEA.
DR	GO; GO:0008270; F:zinc ion binding; IEA.
DR	InterPro; IPR001870; B302.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR006574; PRY.
DR	InterPro; IPR003877; SPRY_receptor.
DR	InterPro; IPR000315; Znf_Box.
DR	InterPro; IPR001841; Znf_Ring.
DR	Pfam; PF00622; SPRY; 1.
DR	Pfam; PF00643; zf-B_box; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00589; PRY; 1.
DR	SMART; SM00184; RING; 1.
DR	SMART; SM00449; SPRY; 1.
DR	PROSITE; PS00290; IG_MHC; 1.
DR	PROSITE; PS01119; ZF_BOX; 1.
DR	PROSITE; PS00518; ZF_RING_1; 1.
DR	PROSITE; PS00089; ZF_RING_2; 1.
SEQ	SEQUENCE 475 AA; 54297 MW; C86750A926E8E434 CRC64;

Query Match 99.5%; Score 2491; DB 11; Length 475;
 Best Local Similarity 99.2%; Pred. No. 8.4e-160;
 Matches 471; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MACSLKDELCSICLSIYQDPVSTGCHYFCRRCITTHWVRQEAGARDCEPCRTTAAEP	60
Dd	1	MACSLKDELCSICLSIYQDPVSTGCHYFCRRCITTHWVRQEAGARDCEPCRTTAAEP	60
Qy	61	ALAPSLXLANIVERYSSFPDLAILNARRAAPCOAHDKVKLFCLTDALLCFFDEPALH	120
Dd	61	ALAPSLXLANIVERYSAFFLDAILNARRAAPCOAHDKVKLFCLTDALLCFFDEPALH	120
Qy	121	EQQVTVTGIDAFDELQBELKDLOALODSREHEFTALQLKRQAETKSSTKSIRTTIGE	180
Dd	121	EQQVTVTGIDAFELQBELKELQALQDSREHEFTALQLKRQAETKSSTKSIRTTIGE	180
Qy	181	AFERLHELLRERQKAMLEELEADPARTLTDTIEQVQVSQOLRKVQEGAQILQERLAETD	240
Dd	181	AFERLHELLRERQKAMLEELEADPARTLTDTIEQVQVSQOLRKVQEGAQILQERLAETD	240
Qy	241	RHTFLAGVASLSERLKGIHETNLTYEDFPFSKYTGPLQYTIWKSLFODIHVPAAULTD	300
Dd	241	RHTFLAGVASLSERLKGIHETNLTYEDFPFSKYTGPLQYTIWKSLFODIHVPAAULTD	300
Qy	301	PGTAHQRLILSDDCCTIVAYGNLHPQIQDSFKPRFDVEVSVLGSAFSGGVHYEWVAEK	360
Dd	301	PGTAHQRLILSDDCCTIVAYGNLHPQIQDSFKPRFDVEVSVLGSAFSGGVHYEWVAEK	360
Qy	361	TQWVIGLAHEAASRGSGTQIQPSRGFYCIVMHDNGQYSACTEPWTRLNVORKLKVGVFL	420
Dd	361	TQWVIGLAHEAASRGSGTQIQPSRGFYCIVMHDNGQYSACTEPWTRLNVORKLKVGVFL	420
Qy	421	DYDQGLLIIFYNADMWSWLTYPREKPGKLCSYFSPGQSHANGKNVQPLINTVRI	475
Dd	421	DYDQGLLIIFYNADMWSWLTYPREKPGKLCSYFSPGQSHANGKNVQPLINTVRI	475

RESULT 4

[illegible]

RESULT 4


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QY 243 TEL----AGVASLSRLKGIHETN-LTYEDPFTSKYTGPLYTKSLFQDIHPVPAAL 297
Db 375 SFLMDIKAFIDKQEOQRAVISTGNTLLSKELCQGTGFGPIQYIMMKELKSVVPSLTPM 434
QY 298 TLDPGTAHORLILSDDDCTIVAYGNLHPQPLQDSPKRFDVEVSVLGSFAFSSGVHYWEVVV 357
Db 435 LLDPTSAHNLHLSGLTSVRYGE-NKLSLPDNPKRFSQCILVLGSGQDGRHYWEV 493
QY 358 AKETQWVIGLAHAASRKSGSIQIOPSRGFCYIVMHDGNOYSACTEPWTRINVRDKLDKVG 417
Db 494 GDKTAWDVGMASESSNRKKGKILNPKNGYWAIWLRNGNAYKALESPSKLSLSSHPRKIG 553
QY 418 VFVDYDQGLLIFYNADMSWLYTFREKFGPKLCSYSPGOSHANGKNVPLR 469
Db 554 VYVDYEGGQISFYNADMTIITFNATFTKLYPYLSP-FLHDSGRKNVDPLR 604

RESULT 5
Q91431
ID Q91431 PRELIMINARY; PRT; 610 AA.
AC Q91431;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nuclear factor 7.
GN XNF7-O.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96081373; PubMed=8541218;
RA Gong S.G., Reddy B.A., Etkin L.D.;
RT "Two forms of Xenopus nuclear factor 7 have overlapping spatial but
RT different temporal patterns of expression during development.";
RL Mech. Dev. 52:305-318(1995).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; S80988; AAB35876.1; -.
DR GO; GO:000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:003682; F:chromatin binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006333; P:chromatin assembly/disassembly; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003649; Bbox C.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00502; BBox; 1.
DR SMART; SM00336; BBox; 1.
DR SMART; SM00298; CHROMO; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 610 AA; 69115 MW; D828F60060572EC1 CRC64;

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Query Match 29.9%; Score 748.5; DB 13; Length 610;
 Best Local Similarity 33.4%; Pred. No. 3.3e-42;
 Matches 159; Conservative 94; Mismatches 198; Indels 25; Gaps 8;
 QY 7 DELLCSICSIYQDPVSLGCEHYFCRRCTTEHWVROEAQGARDPCRCRTFAEPALAPSL 66

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Db 142 EELTCPLCVELFKDPMWACGHNFCSIDKW---EGQSSPACPECKSITDRKYTINR 198
QY 67 KIANIVERYSSPLDAILNARRAARCOAHD-KVKLFCLTDRALLCFDEPALHBOHQV 125
Db 199 VLANLAKAACTVPTVEKKTRPLEKCSHDERLKLCKDDGTGCVICRDSLKHASHNF 258
QY 126 TGIDDAFDELQRE-----LKQQLAQDSEREHEATEALQLKRLQAEKSSKTSLSRTTI 178
Db 259 LPILDAIGVYRELSAIVAPLEASLVTEQLSQSDKIEQHNNKNSVQYKEHWTS----- 313
QY 179 GFAFERLHLRLRQKAMLELEADTARTLTDIEQKVQVRSQQLRVQEGAQLQRLAE 238
Db 314 --EFEKHLKFLKEREKLEQLKEQGNLLTEMNNLVKMQENQDAIKKTIISLAKERMEE 371
QY 239 TRRHTPLAGVASL-----SERLKGKIHTN-LTYEDPFTSKYTGPLYTKSLFQDIHPV 293
Db 372 TDSISFLTDIKTFIDKCOQORAVISTGNTLLSKELCQGTGFGPIQYIMMKELKSVITPS 431
QY 294 PAALTLDPGTAHORLILSDDDCTIVAYGNLHPQPLQDSPKRFDVEVSVLGSFAFSSGVHYW 353
Db 432 LTPMLLDPSAHNLHLSGLTSVRYGE-NKLSLPDNPKRFSQCILVLGSGQDGRHYW 490
QY 354 EVVVAEKTQWVIGLAHAASRKSGSIQIOPSRGFCYIVMHDGNOYSACTEPWTRINVRDKL 413
Db 491 EVEVGDKTAWDVGMASESSNRKKGKILNPKNGYWAIWLRNGNRYKALESPSKALSLSHP 550
QY 414 DKGVFVLDYDQGLLIFYNADMSWLYTFREKFGPKLCSYSPGOSHANGKNVPLR 469
Db 551 RKIGVYVDYEGGQISFYNADMTIITFNATFTKLYPYLSP-FLHDSGRKNVDALR 605

RESULT 6
Q801R9
ID Q801R9 PRELIMINARY; PRT; 453 AA.
AC Q801R9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047956; AAB47956.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003649; Bbox C.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR SMART; SM00502; BBox; 1.
DR SMART; SM00336; BBox; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 453 AA; 51318 MW; B7D93755706B5406 CRC64;

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Query Match 27.7%; Score 693.5; DB 13; Length 453;
 Best Local Similarity 33.1%; Pred. No. 1.1e-38;


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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047945; AAH47945.1; -.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00449; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 500 AA; 57448 MW; 0108A705BD03FDE1 CRC64;

Query Match 24.7%; Score 619; DB 4; Length 500;
Best Local Similarity 31.8%; Pred. No. 1.3e-33;
Matches 149; Conservative 83; Mismatches 221; Indels 16; Gaps 8;

QY 8 ELLGSLICLSIYQDPVSLGCEHYFCRCITTEHWVROEAGARDCEPCRTFAEPALAPSLK 67
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
38 ELHCPLCNDWFRDPLMLSCGHNFCEACIQDFWRLQAKZ--TFCPECKMLCQVNNCTFPV 95
QY 68 LANIVERYSSPFLDAILNARARPCQAH-DKVKLFCLTDRLALLCFDCEPALH--EQHQ 124
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 LDKLVEKIKKLP-----LKGHPQCPHEGNLKLFSKPDGKLCFCQCKDARLSVGQSK 149
QY 125 VTGIDDAFDELQRELKQALQDSEREHTEALQLLKQLAETKSTSLRTTIGEAFER 184
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
150 FLQISDAVHFMEELAIQGGQLETTLKELQTLRNMQKEAIAAHKENKLHQHVSMEFLK 209
QY 185 LHRLLRERQKAMLELEADTARTLTDIEQKVRYSQQLKQVQEGAIQLQERLAETDRHTF 244
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
210 LHQFLHSKEKILYELREGKALNEEMELNSIQEQCLLAKDMLVSIQAKTEQNSDFD 269
QY 245 LAGVASISERLKG--KIHET-NLTVEDPPTSKYTGPLQYTIWKSIFQDIHPVPAALTDLP 301
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
270 LKDIITLLHSLEQGMKVLATRELISKRLNLGQYKGFQYVWVREMQDTLCPGLSLTLDP 329
QY 302 GTAHQRLISDDCTIVAGNLHPQLQDSPKRFDEVSIVLSEAFSSGVHVWVVAEKT 361
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
330 KTAHENLVLSKQTSVMHGDII-KKIMPDPPRFDSSVAVLGSRGFTSGKWYWEVEVAKKT 388
QY 362 QWVIGLAHEAASRKGSIQIOPSRGFYCIVMHDGNQYSACTEPWTRLNVRDLDKVGVFLD 421
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
389 KWTGVVRESIIRKGSCLPTPEQGFLLRLRNQTLKALDLPSPSLTLTNLNDKVGIYLD 448
QY 422 YDQGLLIIFYNADMSWLYTFREKPFGLKCSYFSPGQSHANGKNVQPLRI 470
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
449 YEGQLSFYNAKTHTHIYTSNTEKLYPFCPLND-GGENKEPLHI 496

RESULT 11
Q80X56
ID Q80X56 PRELIMINARY; PRT; 500 AA.
AC Q80X56;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ring finger protein 36.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testicle;
RX MEDLINE=22388257; PubMed=12477932;
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DB 431 PRRSLTGLD-LRRVGVLDYEGGQVSYFNATTMTHTLTYTFSSVFQEKLPFYLCPCLND-GG 488
QY 463 KNVQPLRI 470
DB 489 ENKEPLHI 496

RESULT 12
QVHZ6 PRELIMINARY; PRT; 500 AA.
AC Q8VHZ6;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ring finger-B box-coiled coil transcription factor.
GN RNF36.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21463391; PubMed=11578878;
RA Shyu H., Hsu S., Hsieh-Li H., Li H.;
RT "A novel member of the RBCC family, Trif, expressed specifically in
RT the spermatids of mouse testis.";
RL Mech. Dev. 108:213-216 (2001).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF334958; AAL41031.1; --
DR MGD; MGI:1918178; Rnf36.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 500 AA; 57234 MW; 757907426D8A4E27 CRC64;

Query Match 23.9%; Score 599.5; DB 11; Length 500;
Best Local Similarity 31.1%; Pred. No. 2.8e-32;
Matches 152; Conservative 81; Mismatches 206; Indels 49; Gaps 11;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRRCCITEHHVVRQEAQAGDCEPCRRTFAPALAP 64
DB 36 LTTELHCPCLNDWFRDPLMTGHNFCQDCIQSFVKVHSKE--TFCDCKMLQYSNCTF 93
QY 65 SLKLANIVERYSPFLDAILNARRAAPCOAH-DKVKLFCLTDRLALCFCDPEPALHEQ 123
DB 94 NLVLEKIVKIKLPL-----LKGHPQCAEHGKLNKLFKPEGMICFOCKDARLS--- 144
QY 124 QVTGIDDAFDELQELKDQALQDSEREHTEALQLLKRLAETKSTKSLRTTIGEAF-- 181
DB 145 -----MGQSKDFLQ--ISEAVRFTTELAIQSLOTTLKELOSLRTIQKDAIS 191
QY 182 -----PERLHLLRERQKAMLELEADTARTLTLDIQKVQRYSQLRKV 225
DB 192 AYKDNKIQLOONLSLEFLKHLQFHNKEKIDLNDLRDEGKLLNEEMVNLQEOCLVA 251
QY 226 QEGAQILQELAEADRTHTFLAGVASISERL-KG--KIHETNLTYEDPTSKYTGPIQYTI 282
DB 252 KDLMTATQARMEQONSDFLTDITKLTJESMEKGMKTIIVPRLIAKLSLGRFKGPIQYII 311
QY 283 WKSIFQDIHVPAAITLDPCTAHQRLTSDDCITVAGNLHPQLQDSPKRFDEVSVLG 342
DB 312 WKEMQAILSPGSQLTLDPKTAHPNLVLSKTSQTSVCHCDV--KQVLPDPPERLSSVAVLG 370

343 SEAFSSGVHYWVWVAEKTQWVIGLAHEAASRKSIIQIPSRGFYCI VMHDGNQVSACTE 402
DB 371 SKGFTSGRWYWEIEVGKTKTWIGVVRESIIKSGCPLTPEQGFLLRLNRNQTDLKALDL 430
QY 403 PWTRLNVRDKLQKGVFLDYDQGLLIFYNADMSMLYTFREKFPKGLCSYFSPGQSHANG 462
DB 431 PRRSLTGLD-LRRVGVLDYEGGQVSYFNATTMTHTLTYTFSSVFQEKLPFYLCPCLND-GG 488
QY 463 KNVQPLRI 470
DB 489 ENKEPLHI 496

RESULT 13
Q810I2 PRELIMINARY; PRT; 483 AA.
AC Q810I2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tripartite motif protein 50.
GN TRIM50.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ucla C., Meria G., Meroni G., Raymond A.;
RT "Novel genes in the Williams-Beuren Syndrome critical region.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY081947; AAL91070.1; --
DR GO; GO:0005622; C-intracellular; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR00315; Znf_Ebox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 483 AA; 54607 MW; DA3A7234C1A8145B CRC64;

Query Match 23.7%; Score 593; DB 11; Length 483;
Best Local Similarity 30.4%; Pred. No. 7.3e-32;
Matches 145; Conservative 83; Mismatches 217; Indels 32; Gaps 10;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRRCCITEHHVVRQEAQAGDCEPCRRTFAPALAP 64
DB 10 LQDLQCPICLEVKEPLMLQCGHSYCKDCLDN--LSQHLDSLELCCPCRCQSDCSSPP 67
QY 65 SLKLANIVERYSPFLDAILNARRAAPCOAH-DKVKLFCLTDRLALCFCDPEPALHEQ 122
DB 68 NVSLARVI-----DALFLPGDIBFTVCVHHRNPLSLFCEKDQBFICGLGGLGSHQH 119
QY 123 HQVTGIDDAFDELQELKDQALQDSEREHTEALQLLKRLAETKSTKSLRTTIGEAF 182
DB 120 HRVTPVSTVSRMKELAGRISELKEHNRVEEHGKLVNRRTRIINESDVFSWVIRREF 179
QY 183 ERLHLLRERQKAMLELEADTARTLTLDIQKVQRYSQLRKVQEGAIILQERLAETDRH 242
DB 180 QELHHLVDEEKARCLEGLEHTRGLVASLDMQLEQAQGTQERLAQAEQVL--EQFGNSHH 238
QY 243 TELAA--GVASLSRELKGIHETNLTYEDFTSKYTGPIQVTKSLFQDHPVPAALTLTD 300
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Db 239 EFIRFHSVASRAEVQOARPLEGVFSPISFKPALHQADIKLTVKRLFRKVLPAASLKLD 298
QY 301 PCTAHQRLILSDCTIVAYGNLHPQLQSPKRFDEVEVSLGSEAFSSGVHYWVVAEK 360
Db 299 PATAHPLLELSKGNIVVHCG-LLAQRASQPERFDYSTCVLASKGSFGRHYWVVGSK 357
QY 361 TOWVIGLAHEAASRKSGSIQIOPSRGFCYCIVMHDGNOYSACTBPWTRLNVRDLDKVGVEL 420
Db 358 SDWRLGVKGTASRKGLNKSPEHGWLLGLKEGRVYEAFCGPRPLPVAGHPHRIGVYL 417
QY 421 DYDQGLLIIFYNA---DDMSWLYTFREKPEPKL-----CSYFSPGOSHANGKVVQL 468
Db 418 HYEQELTEFFDADRPDDLRTLYTFQADFQGLYPILDTCT-----WHERGNSLPM 467

RESULT 14
Q81011
ID Q81011 PRELIMINARY; PRT; 483 AA.
AC Q81011;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tripartite motif protein 50.
GN TRIM50.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Ucla C., Merla G., Meroni G., Reymond A.;
RT "Novel genes in the Williams-Beuren Syndrome critical region.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY081950; AAL91073.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf Box.
DR InterPro; IPR001841; Znf Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 483 AA; 54719 MW; 2C9171E12902AEAF CRC64;

Query Match 23.5%; Score 588; DB 11; Length 483;
Best Local Similarity 30.2%; Pred. No. 1.6e-31;
Matches 147; Conservative 81; Mismatches 207; Indels 52; Gaps 11;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGDCPECRRTFAEPALAP 64
Db 10 LQDQLQPCICLEVKEPLMLQCGHSYCKNCLDS--LSEHLDSLELRCPVCQSVDCSSSP 67
QY 65 SLKLANIVERSYSPFLDAI-LNARRAAPCOAH-DKVKLFCLTDRALLCFPCDEPALHEQ 122
Db 68 NVSLARVI-----DALRLPGTEPTVCVHHRNPLSLFCEKQDEFTICGLLGHSHQ 119
QY 123 HOVTGIDDAFDELORELKDQALQDSEREHTEALQLKROLATKSTKSLRTTIGAEF 182
Db 120 HRVTPSVTVSRMKELEADTARTLTDIEQVQVYQSLRKVQEGAGIQLERLAETDR- 179
QY 183 ERLHLRLRQKAMLELEADTARTLTDIEQVQVYQSLRKVQEGAGIQLERLAETDR- 241
Db 180 QELHLVDEEKARCLEGVESHTRGLVASLDMQL-----EQAQGTQERLAQAERY 228
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QY 242 -----HTFLA--GVASLSERLKGKIHTNLTIVEDPTPTKYTPLOYYTIWKSILFQDI 290
Db 229 LEQFQNESHEFIRFHSITSRGEVQOARPLEGVFSPISFKPALHQADIKLTVKRLFRKV 288
QY 291 HVPAAALTDPCGTAHQRLILSDCTIVAYGNLHPQLQSPKRFDEVEVSLGSEAFSSGV 350
Db 289 LEAPESLKLDPATAHPLLELSKGNIVVHCG-LLAQRASQPERFDYSTCVLASKGSFGR 347
QY 351 HYWVVAEKTOWVIGLAHEAASRKSGSIQIOPSRGFCYCIVMHDGNOYSACTBPWTRLNVR 410
Db 348 HYWVVGVSQSWRLGVKGTASRKGLNKSPEHGWLLGLKEGRYEAFCGPRPLPVLA 407
QY 411 DKLDKVGVELDYDQGLLIIFYNA---DDMSWLYTFREKPEPKL-----CSYFSPGOSHAN 461
Db 408 GHPHRIGVLYHYEQELTEFFDADRPDDLRTLYTFQADFQGLYPILDTCT-----WHER 460
QY 462 GKNVQPL 468
Db 461 GNSLPM 467

RESULT 15
Q865W2
ID Q865W2 PRELIMINARY; PRT; 486 AA.
AC Q865W2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tripartite motif protein 50.
GN TRIM50.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Ucla C., Merla G., Meroni G., Reymond A.;
RT "Novel genes in the Williams-Beuren Syndrome critical region.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY081951; AAL91074.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf Bbox.
DR InterPro; IPR001841; Znf Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 486 AA; 54775 MW; A33ABD06EFC7A7F1 CRC64;

Query Match 23.2%; Score 581; DB 6; Length 486;
Best Local Similarity 29.4%; Pred. No. 4.7e-31;
Matches 141; Conservative 82; Mismatches 220; Indels 36; Gaps 10;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGDCPECRRTFAEPALAP 64
Db 10 LEDRLQPCVCLVKEPLMLQCGHSYCKGCLLS--LSRHLDSELRCPVCQFVDSSSSP 67
QY 65 SLKLANIVERSYSPFLDAI-LNARRAAPCOAH-DKVKLFCLTDRALLCFPCDEPALHEQ 123
Db 68 NVSLARVIALQ-----LPGDPEPQVCTHHRNPLSLFCEKQDEFTICGLLGHSHQ 120
QY 124 QVTGIDDAFDELORELKDQALQDSEREHTEALQLKROLATKSTKSLRTTIGAEF 183
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Db 121 RVPVSTVYSRMKEELALISDLKQEQKVEQVAKLVNNRTRIYNESDVFSWVIRREFQ 180
Qy 184 RIHRLRERQKAMLELEADTARTITDIEQKVQRYQQIRKVQE---GAQILQERLAETD 240
Db 181 ELHLVDEEKARCLEGVEGHTRGVLVASLDMQL---EQARGAQERLAQATCMLEQFGNES 236
Qy 241 RHTFLA--GVASLSERLKGKIHETNLTIEDPFTSKYTGPELOYTIWKSIFQDHPVPAALT 298
Db 237 HYEFTIRYHSTASSAELOQARLLEGAFSPISFKPLHQADIKLTVWKRJFRKVLPAPELX 296
Qy 299 LDPEGAHORLILSDDCITIVAYGNLHPQPLQDQPKRFDVEVSVLGSEAFSSGVHYWEVVVA 358
Db 297 LDFTTAHPLLELSKGNVTVVQCG-LLAQRRASQPERDYSTCVLASRGFSCGRHYWEVVVG 355
Qy 359 EXTQWVIGLAHEAARKGSIQIOPSRGFYCIWMHDGNQYSACTEPWTRLNVRDKLDKGVV 418
Db 356 SKSDWELGVIKGTASRKGLNKSPHGVWLI GLKEGRVYEAFSCPRVPLPVAGHPHRIGV 415
Qy 419 FLDYDQGLLIFVNA---DDMSWLYTFREKFPQKL-----CSYFSPQSHANGKNVQPL 468
Db 416 YLHYBQGEITFFDADRPDDLRLLYTFQADFOGKLYPILDTC-----WHERGSNSLPM 467

Search completed: July 23, 2004, 15:07:40
Job time : 44 secs